

STIC-Biotech/ChemLib

173147

From: Bowman, Amy
Sent: Friday, December 02, 2005 9:43 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: FW: sequence search-10/773,678

Hello, this is the search that I requested earlier today. It has been approved for a rush.
Thanks so much for your help,
Amy Bowman

-----Original Message-----

From: Richter, Johann
Sent: Friday, December 02, 2005 9:39 AM
To: Bowman, Amy
Cc: STIC-Biotech/ChemLib
Subject: RE: sequence search-10/773,678

Approved.

Johann R. Richter, Ph.D., Esq.
Supervisory Patent Examiner
Biotechnology and Organic Chemistry
Art Unit 1621
571-272-0646

-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 9:08 AM
To: Richter, Johann
Cc: Bowman, Amy
Subject: FW: sequence search-10/773,678

-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 9:07 AM
To: Chan, Christina; Hutzell, Paula
Subject: FW: sequence search-10/773,678

Hello,
My SPE, Drew Wang, thought I should ask for a rush search for this case. Am I contacting the appropriate person to request this?
Thank you,
Amy Bowman

Point of Contact
P. Sheppard

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

RECEIVED
DEC - 2 2005
STIC/BIOTECH. DIV. (STIC)

12/05/05
JH

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-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 8:54 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: FW: sequence search-10/773,678

I meant to mention that this case is about to be allowed, so I will need to include the interference database...

-----Original Message-----

From: Bowman, Amy
Sent: Friday, December 02, 2005 7:31 AM
To: STIC-Biotech/ChemLib
Cc: Bowman, Amy
Subject: sequence search-10/773,678

Hello,
I need a search of SEQ ID NO: 342 in application 10/773,678, length limited to 30 nucleobases.
Thank you,
Amy Bowman
AU 1635
REM 2C31
mail REM 2C18
571-272-0755

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:02:55 ; Search time 2155 Seconds
(without alignments)
527.549 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactcttcgaggaagcggt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 1641224

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_px.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vl.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	80.0	20	6	CQ979199 Sequence
2	14	70.0	20	6	AR120998 Sequence
3	14	70.0	20	6	BD272619 Antisense
4	14	70.0	20	6	AR531367 Sequence
5	13.8	69.0	25	6	AX043113 Sequence
6	13.8	69.0	28	6	AR205609 Sequence
7	13.4	67.0	24	6	AX446884 Sequence
8	13	65.0	19	4	DOGPA45501
9	13	65.0	26	6	AX554614 Sequence
10	13	65.0	26	6	AX703339 Sequence
11	12.8	64.0	20	6	BD228539 IL-17 hom
12	12.8	64.0	20	6	AR359764 Sequence
13	12.8	64.0	27	6	A98434 Sequence 18
14	12.8	64.0	30	6	AX576339 Sequence
15	12.6	63.0	20	6	C0798932 Sequence
16	12.6	63.0	21	6	CQ893797 Sequence
17	12.6	63.0	21	6	AR361504 Sequence
18	12.6	63.0	23	6	AR081003 Sequence

19	12.6	63.0	23	6	I60352
c 20	12.6	63.0	24	6	AX292865
21	12.6	63.0	25	6	CQ628266
22	12.6	63.0	25	6	CQ628267
23	12.6	63.0	25	6	CQ628268
24	12.6	63.0	25	6	CQ628269
25	12.6	63.0	25	6	CQ628270
26	12.6	63.0	25	6	CQ628271
27	12.6	63.0	25	6	CQ628272
28	12.6	63.0	25	6	AR469329
29	12.6	63.0	25	6	AR469330
30	12.6	63.0	25	6	AR469331
31	12.6	63.0	25	6	AR469332
32	12.6	63.0	25	6	AR469333
33	12.6	63.0	25	6	AR469334
34	12.6	63.0	25	6	AR469335
c 35	12.6	63.0	26	6	BD133366
36	12.6	63.0	30	6	AR172849
37	12.6	63.0	30	6	AX081299
38	12.4	62.0	17	6	A89364
39	12.4	62.0	17	6	BD066877
40	12.4	62.0	17	6	AX762730
41	12.4	62.0	17	6	AX762313
42	12.4	62.0	18	6	AX117443
c 43	12.4	62.0	20	6	AR098941
c 44	12.4	62.0	20	6	AR164768
c 45	12.4	62.0	20	6	BD222879

ALIGNMENTS

RESULT 1
CQ979199 CQ979199 20 bp DNA linear PAT 19-JAN-2005
LOCUS Sequence 201 from Patent WO2004111273.
ACCESSION CQ979199
VERSION CQ979199.1 GI:57976452
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS other sequences; artificial sequences.
TITLE
JOURNAL
Agus, D., Baker, J.B., Natale, R. and Shak, S.
Gene expression markers for response to egfr inhibitor drugs
Patent: WO 2004111273-A 201 23-DEC-2004;
Genomic Health, Inc. (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="reverse primer"

ORIGIN

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 CTTGCAGGAGCGGCT 20
Db 1 CTTGCAGGAGCGGCT 16
RESULT 2
AR120998 AR120998 20 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 19 from patent US 6159694.
DEFINITION
ACCESSION AR120998
VERSION AR120998.1 GI:14104574
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Karas, J.G.
TITLE Antisense modulation of stat3 expression
JOURNAL Patent: US 6159694-A 19 12-DEC-2000;
FEATURES Location/Qualifiers
    source 1..20
           /organism="unknown"
           /mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACTCTTGCAGGAA 14
   |||||
Db 7 GACTCTTGCAGGAA 20

RESULT 3
LOCUS BD272619 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense oligonucleotide modulation of STAT3 expression.
ACCESSION BD272619
VERSION BD272619.1 GI:33082387
KEYWORDS JP 2002541784-A/19
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Karas, J.G.
TITLE Antisense oligonucleotide modulation of STAT3 expression
JOURNAL Patent: JP 2002541784-A 19 10-DEC-2002;
COMMENT ISIS PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2002541784-A/19
PD 10-DEC-2002
PF 06-APR-2000 JP 2000611544
PR 08-APR-1999 US 09/288461
PI JAMES G KARRAS
PC C12N15/09,A61K31/711,A61K48/00,A61P29/00,A61P35/00,
PC A61P37/02,
PC A61P43/00,C12N5/06,C12Q1/02,C12N15/00,C12N5/00 CC Antisense
oligonucleotide
FH Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
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           Location/Qualifiers
           1..20
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           /db_xref="taxon:32630"
ORIGIN
Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACTCTTGCAGGAA 14
   |||||
Db 7 GACTCTTGCAGGAA 20

RESULT 4
LOCUS AR531367 20 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 19 from patent US 6727064.
ACCESSION AR531367
VERSION AR531367.1 GI:53919806
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Karas, J.G.
TITLE Antisense oligonucleotide modulation of STAT3 expression
JOURNAL Patent: US 6727064-A 19 27-APR-2004;
FEATURES Location/Qualifiers
    source 1..20
           /organism="unknown"
           /mol_type="genomic DNA"
ORIGIN
Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.2e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACTCTTGCAGGAA 14
   |||||
Db 7 GACTCTTGCAGGAA 20

RESULT 5
LOCUS AX043113 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 679 from Patent WO0065088.
ACCESSION AX043113
VERSION AX043113.1 GI:11341721
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Ulfendahl, P.J. and Wong, K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 679 02-NOV-2000;
COMMENT Amersham Pharmacia Biotech AB (SE)
FEATURES
    source 1..25
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="DPA1 Heterozygote Primer Sequence"
ORIGIN
Query Match 69.0%; Score 13.8; DB 6; Length 25;
Best Local Similarity 88.2%; Pred. No. 9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCTTGCAGGAAGCGGCT 20
   |||||
Db 9 TTTTGCAGGAAGAGGCT 25

RESULT 6
LOCUS AR205609 28 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 13 from patent US 6369038.
ACCESSION AR205609
VERSION AR205609.1 GI:21503235
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Blumenfeld, M., Brandys, P., d'Auriol, L. and Vasseur, M.
TITLE Closed antisense and sense oligonucleotides and their applications
JOURNAL Patent: US 6369038-A 13 09-APR-2002;
FEATURES Location/Qualifiers
    source 1..28
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           /mol_type="unassigned DNA"
ORIGIN
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Query Match      69.0%; Score 13.8; DB 6; Length 28;
Best Local Similarity 88.2%; Pred. No. 8.9e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 CTCTTGCAGGAAGCGGC 19
    ||||| ||||| |||||
Db 12 CTCTTGCAGGAAGCGGC 28

RESULT 7
AX446884
LOCUS AX446884 24 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 3339 from Patent WO0216649.
ACCESSION AX446884
VERSION AX446884.1 GI:21695783
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Gunderson,K.
TITLE Probes and decoder oligonucleotides
JOURNAL Patent: WO 0216649-A 3339 28-FEB-2002;
Illumina, Inc. (US)
FEATURES
source Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."

ORIGIN
Query Match      67.0%; Score 13.4; DB 6; Length 24;
Best Local Similarity 93.3%; Pred. No. 1.4e+05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TTGCAGGAAGCGGCT 20
    ||||| ||||| |||||
Db 6 TGCAGGAAGCGGCT 20

RESULT 8
DOGP45501
LOCUS DOGP45501 19 bp DNA linear MAM 22-JAN-1996
DEFINITION Dog (Clone: CXK.455) primer for STS 455, 5' end.
ACCESSION L24340
VERSION L24340.1 GI:402053
KEYWORDS PCR identification; PCR primer; STS.
SEGMENT 1 of 2
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (Bases 1 to 19)
Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
One hundred and one new simple sequence repeat-based markers for
the canine genome
Mamm. Genome 6 (3), 192-195 (1995)
JOURNAL 7749226
PUBMED Original source text: Canis familiaris (library: E. Ostrander, in
pBluescript+) adult spleen DNA.
Submitted by:
Fred Hutchinson Cancer Research Center
Transplantation Biology Dept
1124 Columbia; Mailstop M318
Seattle, WA 98104, USA
e-mail: EOostrander@hlbi.gov
PCR Buffer: PCR buffer (Perkin-Elmer/Cetus)
PCR Profile: Denaturation: 94 degrees C for 1.00 minute
Annealing: 55 or 59 degrees C for 0.45 minutes
Polymerization: 74 degrees C for 1.00 minutes
PCR Cycles: 33

Final Extension: 74 degrees C for 5.00 minutes.
Location/Qualifiers
1..19
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/tissue_type="spleen"
/dev_stage="adult"
/tissue_lib="E. Ostrander, in pBluescript+"

ORIGIN
Query Match      65.0%; Score 13; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGC 16
    ||||| ||||| |||||
Db 4 TCTTGCAGGAAGC 16

RESULT 9
AX554614
LOCUS AX554614 26 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 168 from Patent WO0246229.
ACCESSION AX554614
VERSION AX554614.1 GI:25898281
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Casman,S.J., Padigaru,M., Burgess,C.E., Shimkets,R.A., Spytek,K.A.,
Gilbert,J.A., Mayotte,J.E., Baumgartner,J.C., Mishra,V.,
Vernet,C.A., Dickinson,K.S., Ballinger,R.A. and Wolenc,A.R.
Novel proteins and nucleic acids encoding same
Patent: WO 0246229-A 168 13-JUN-2002;
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1..26
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="PCR Primer Sequence"

ORIGIN
Query Match      65.0%; Score 13; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGC 16
    ||||| ||||| |||||
Db 3 TCTTGCAGGAAGC 15

RESULT 10
AX703339
LOCUS AX703339 26 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 568 from Patent WO02059313.
ACCESSION AX703339
VERSION AX703339.1 GI:29538385
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Li,L., Ballinger,R.A., Padigaru,M., Kekuda,R., Colman,S.D.,
Spytek,K.A., Casman,S.J., Vernet,C.A., Shenoy,S.G., Gusev,V.,
Malyankar,U.M., Edinger,S., Gerlach,V., Smithson,G., Stone,D.J.,
Sciore,P., Macdougall,J.R., Gunther,E., Peyman,J.A., Ellerman,K.,
Gangolli,E.A. and Willet,I.
G-protein coupled receptors and nucleic acids encoding same
Patent: WO 02059313-A 568 01-AUG-2002;
JOURNAL
```

RESEARCH	Schaezel, H.
AUTHORS	Prion protein dimers useful for vaccination
TITLE	Patent: EP 1251138-A 14 23-OCT-2002;
JOURNAL	Schaezel, Hermann (DE)
FEATURES	Location/Qualifiers

ORIGIN

LOCUS I60352 23 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 86 from patent US 5656427.
ACCESSION I60352
VERSION I60352.1 GI:2478797
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hammond, P.W. and Endozo, A.A.
TITLE Nucleic acid hybridization assay probes, helper probes and amplification oligonucleotides targeted to Mycoplasma pneumoniae nucleic acid
JOURNAL Patent: US 5656427-A 86 12-AUG-1997;
FEATURES source
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/mol_type="unassigned DNA"
ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 23;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GACTCTTGCAGGAAGCGGC 19
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Db 5 GACTCTAGCAGGCAATGCG 23
RESULT 20
AX292865/c
LOCUS AX292865 24 bp DNA linear PAT 21-NOV-2001
DEFINITION Sequence 4627 from Patent WO0179548.
ACCESSION AX292865
VERSION AX292865.1 GI:17054548
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Barany, F., Zirvi, M., Gerry, N.P., Favis, R. and Kliman, R.
TITLE Method of designing addressable array for detection of nucleic acid sequence differences using ligase detection reaction
JOURNAL Patent: WO 0179548-A 4627 25-OCT-2001;
CORNELL RESEARCH FOUNDATION, INC. (US)
FEATURES source
1. .24
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Hypothetical Probe Sequence"
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Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ACTCTTGCAGGAAGCGGCT 20
||||| ||||| |||||
Db 23 ACTGCTGCACTAAGCGGCT 5
RESULT 21
CQ628266
LOCUS CQ628266 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13006 from Patent WO0192524.
ACCESSION CQ628266
VERSION CQ628266.1 GI:41678484
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13006 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES source
1. .25
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ACTCTTGCAGGAAGCGGCT 20
||||| ||||| |||||
Db 7 AGTCTGCCAGAAAGCGGCT 25
RESULT 22
CQ628267
LOCUS CQ628267 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13007 from Patent WO0192524.
ACCESSION CQ628267
VERSION CQ628267.1 GI:41678485
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle
JOURNAL Patent: WO 0192524-A 13007 06-DEC-2001;
Aeomica, Inc. (US)
FEATURES source
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Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 2 ACTCTTGCAGGAAGCGGCT 20
||||| ||||| |||||
Db 6 AGTCTGCCAGAAAGCGGCT 24
RESULT 23
CQ628268
LOCUS CQ628268 25 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 13008 from Patent WO0192524.
ACCESSION CQ628268
VERSION CQ628268.1 GI:41678486
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
REFERENCE 1
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Myosin-like gene expressed in human heart and muscle

FEATURES

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Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGCGGCT 20
Db 1 AGTCCTGCCAGAGCGGCT 19

RESULT 28
AR469329
LOCUS AR469329 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13006 from patent US 6686188.
ACCESSION AR469329
VERSION AR469329.1 GI:42704386
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13006 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGCGGCT 20
Db 7 AGTCCTGCCAGAGCGGCT 25

RESULT 29
AR469330
LOCUS AR469330 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13007 from patent US 6686188.
ACCESSION AR469330
VERSION AR469330.1 GI:42704387
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13007 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
FEATURES
source Location/Qualifiers
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/mol_type="genomic DNA"
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Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGCGGCT 20
Db 6 AGTCCTGCCAGAGCGGCT 24

Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 30
AR469331
LOCUS AR469331 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13008 from patent US 6686188.
ACCESSION AR469331
VERSION AR469331.1 GI:42704388
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13008 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
FEATURES
source Location/Qualifiers
1..25
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/mol_type="genomic DNA"
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Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGCGGCT 20
Db 5 AGTCCTGCCAGAGCGGCT 23

RESULT 31
AR469332
LOCUS AR469332 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13009 from patent US 6686188.
ACCESSION AR469332
VERSION AR469332.1 GI:42704389
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13009 03-FEB-2004; Amersham PLC; Buckinghamshire; GBX;
FEATURES
source Location/Qualifiers
1..25
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/mol_type="genomic DNA"
ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAAGCGGCT 20
Db 4 AGTCCTGCCAGAGCGGCT 22

RESULT 32
AR469333
LOCUS AR469333 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13010 from patent US 6686188.
ACCESSION AR469333
VERSION AR469333.1 GI:42704390
```

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu.Y., Ji.Y., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13010 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES Location/Qualifiers
source 1..25
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/mol_type="genomic DNA"
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Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 ACTCTTCAGGAGCGGCT 20
Db 3 AGTCCTGCCAGAGCGGCT 21
RESULT 33
AR469334
LOCUS AR469334 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13011 from patent US 6686188.
ACCESSION AR469334
VERSION AR469334.1 GI:42704391
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu.Y., Ji.Y., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.
TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13011 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 ACTCTTCAGGAGCGGCT 20
Db 2 AGTCCTGCCAGAGCGGCT 20
RESULT 34
AR469335
LOCUS AR469335 25 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 13012 from patent US 6686188.
ACCESSION AR469335
VERSION AR469335.1 GI:42704392
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Gu.Y., Ji.Y., Penn.S.G., Hanzel,D.K., Rank,D.R., Chen,W. and Shannon,M.E.

TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
JOURNAL Patent: US 6686188-A 13012 03-FEB-2004;
Amersham PLC; Buckinghamshire;
GBX;
FEATURES Location/Qualifiers
source 1..25
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 25;
Best Local Similarity 78.9%; Pred. No. 3.7e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 ACTCTTCAGGAGCGGCT 20
Db 1 AGTCCTGCCAGAGCGGCT 19
RESULT 35
BD133366/c
LOCUS BD133366 26 bp DNA linear PAT 18-SEP-2002
DEFINITION Amino acid sequence of antigen epitope recognized by anticancer human monoclonal antibody CLN-IgG and DNA nucleotide sequence encoding it.
ACCESSION BD133366
VERSION BD133366.1 GI:23228311
KEYWORDS JP 2002051785-A/9.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Hagiwara,H. and Aotsuka,Y.
TITLE Amino acid sequence of antigen epitope recognized by anticancer human monoclonal antibody CLN-IgG and DNA nucleotide sequence
JOURNAL Patent: JP 2002051785-A 9 19-FEB-2002;
YOSHIIHIDE HAGIWARA,HIDEAKI HAGIWARA
COMMENT OS Artificial Sequence
PN JP 2002051785-A/9
PD 19-FEB-2002
PF 09-AUG-2000 JP 2000241927
PI HIDEAKI HAGIWARA,YASUYUKI AOTSUKA
PC C12N15/09,C07K14/82//C12N1/21,(C12N1/21,C12R1:19),C12N15/00 CC
To synthesize while referring to the sequence of human CC vimentin
FH Key Location/Qualifiers
FT source 1..26
/organism="Artificial Sequence".
FEATURES Location/Qualifiers
source 1..26
/organism="synthetic construct"
/mol_type="genomic DNA"
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ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 26;
Best Local Similarity 78.9%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GACTCTTCAGGAGCGGC 19
Db 22 GCCGCTTCAGGATGCGGC 4
RESULT 36
AR172849
LOCUS AR172849 30 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 8 from patent US 6303365.
ACCESSION AR172849
VERSION AR172849.1 GI:17912340
KEYWORDS Unknown.
SOURCE Unknown.

```
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Martin,W.Frank., Hain,R., Tietjen,K.-G., Busch,M. and Kloti,A.S.
TITLE Method of determining activity of 1-deoxy-D-xylulose-5-phosphate
reductoisomerase and 1-deoxy-D-xylulose-5-phosphate synthase
JOURNAL Patent: US 6303365-A 8 16-OCT-2001;
FEATURES Location/Qualifiers
source 1..30
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 30;
Best Local Similarity 78.9%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCGGC 19
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Db 8 GACTCATGCATGAACGTCG 26

RESULT 37
AX081299 30 bp DNA linear PAT 27-FEB-2001
LOCUS Sequence 8 from Patent WO0109341.
DEFINITION AX081299
ACCESSION AX081299
VERSION AX081299.1 GI:13170149
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1
AUTHORS Hain,R., Tietjen,K.G., Busch,M., Martin,W.F. and Kloeti,A.S.
TITLE Method of determining the activity of
1-deoxy-d-xylulose-5-phosphate reductoisomerase and
1-deoxy-d-xylulose-5-phosphate synthase
JOURNAL Patent: WO 0109341-A 8 08-FEB-2001;
Bayer Aktiengesellschaft (DE)
FEATURES Location/Qualifiers
source 1..30
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"

ORIGIN
Query Match 63.0%; Score 12.6; DB 6; Length 30;
Best Local Similarity 78.9%; Pred. No. 3.6e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCGGC 19
||||| ||||| ||| |||
Db 8 GACTCATGCATGAACGTCG 26

RESULT 38
A89364
LOCUS Sequence 1512 from Patent WO9833904.
DEFINITION A89364
ACCESSION A89364
VERSION A89364.1 GI:6737934
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
unclassified sequences.
1 (bases 1 to 17)
Brysch,W. and Schlingensiepen,K.
REFERENCE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
AUTHORS TITLE
JOURNAL Patent: WO 9833904-A 1512 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES Location/Qualifiers
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 62.0%; Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. No. 4.7e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAAG 15
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Db 4 ACTCTTGCAGGTAG 17

RESULT 39
BD066877 17 bp DNA linear PAT 27-AUG-2002
LOCUS An antisense oligonucleotide preparation method.
DEFINITION BD066877
ACCESSION BD066877
VERSION BD066877.1 GI:22612480
KEYWORDS JP 2001511000-A/1512.
SOURCE unidentified
ORGANISM unidentified
unclassified.
1 (bases 1 to 17)
Schlingensiepen,K.H. and Brysch,W.
REFERENCE An antisense oligonucleotide preparation method
AUTHORS TITLE
JOURNAL Patent: JP 2001511000-A 1512 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1512
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PI 31-JAN-1997 EP 97101531.8
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
FT source 1..17
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FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 62.0%; Score 12.4; DB 6; Length 17;
Best Local Similarity 92.9%; Pred. No. 4.7e+05;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAAG 15
||||| ||||| |||
Db 4 ACTCTTGCAGGTAG 17

RESULT 40
AX672730 17 bp DNA linear PAT 27-MAR-2003
LOCUS Sequence 1175 from Patent WO03004526.
DEFINITION AX672730
ACCESSION AX672730
VERSION AX672730.1 GI:29331078
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Teleman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
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JOURNAL medicines
 Patent: WO 03004526-A 1175 16-JAN-2003;
 Molecular Engines Laboratories (FR)
 FEATURES Location/Qualifiers
 source 1..17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 62.0%; Score 12.4; DB 6; Length 17;
 Best Local Similarity 92.9%; Pred. No. 4.7e+05;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGGCT 20

Db 3 TCCAGGAAGCGGCT 16

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 Job time : 2157 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 11:16:05 ; Search time 476 Seconds
(without alignments)
280.029 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactcttgacgaagcggct 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 4138570

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001as.*
- 5: Geneseq2001bs.*
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- 7: Geneseq2002bs.*
- 8: Geneseq2003as.*
- 9: Geneseq2003bs.*
- 10: Geneseq2003cs.*
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- 12: Geneseq2004as.*
- 13: Geneseq2004bs.*
- 14: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	ADZ11151	Adz11151 Human STA
2	20	100.0	29	ADZ10967	Adz10967 Human STA
3	19	95.0	20	ADZ10988	Adz10988 Human STA
4	19	95.0	20	ADZ11150	Adz11150 Human STA
5	18	90.0	20	ADZ11152	Adz11152 Human STA
6	17	85.0	20	ADZ11149	Adz11149 Human STA
7	17	85.0	20	ADZ11153	Adz11153 Human STA
8	16	80.0	20	ADW26449	Adw26449 EGFR inh
9	15	75.0	20	ADZ11154	Adz11154 Human STA
10	15	75.0	20	ADZ11148	Adz11148 Human STA
11	14.4	72.0	29	AA78506	Aat78506 Thiol-spe
12	14	70.0	20	AA93168	Aac93168 Human STA
13	14	70.0	20	AA596785	Aas96785 Human STA
14	14	70.0	20	ADZ10828	Adz10828 Human STA
15	13.8	69.0	25	AA96250	Aac96250 HLA DPA1
16	13.8	69.0	28	AAQ31029	Aaq31029 Circular
17	13.6	68.0	20	ADMI4825	Admi4825 Human mPG
18	13.6	68.0	30	ADR45889	Adr45889 PCR prime
19	13.6	68.0	30	ADR45885	Adr45885 PCR prime

20	13.6	68.0	30	13	ADR45887	Adr45887 PCR prime
21	13.4	67.0	24	6	ABQ03332	Abq03332 Oligonucle
22	13.2	66.0	23	3	AAZ89440	Aaz89440 Human typ
23	13.2	66.0	25	12	ADH72962	Adh72962 M. tuberc
24	13	65.0	15	4	AAF46591	Aaf46591 IGFBP3 ol
25	13	65.0	15	4	AAF46590	Aaf46590 IGFBP3 ol
26	13	65.0	15	4	AAF46589	Aaf46589 IGFBP3 ol
27	13	65.0	25	12	ADP14476	Adp14476 Renal cel
28	13	65.0	26	6	ABS59220	Abs59220 Human G-p
29	13	65.0	26	6	ABT04530	Abt04530 Human G-p
30	13	65.0	26	6	ABT05715	Abt05715 GPCR rela
31	13	65.0	26	12	ADH31280	Adh31280 Human G-p
32	12.8	64.0	24	12	ADK98351	Adk98351 Primer of
33	12.8	64.0	25	9	AC112520	Ac112520 Human mic
34	12.8	64.0	25	9	ACH63464	Ach63464 DNA targe
35	12.8	64.0	25	9	ACH51423	Ach51423 DNA targe
36	12.8	64.0	25	9	ACH53400	Ach53400 DNA targe
37	12.8	64.0	27	2	AA222793	Aax222793 PCR prime
38	12.8	64.0	27	10	ADC51654	Adc51654 5' PCR pr
39	12.8	64.0	30	10	ABZ21923	Abz21923 Mouse fus
40	12.6	63.0	20	12	ADM92376	Adm92376 Pancreat
41	12.6	63.0	20	12	ADM14384	Adm14384 Human mPG
42	12.6	63.0	20	12	ADM14826	Adm14826 Human mPG
43	12.6	63.0	21	11	ADP19693	Adp19693 Periodont
44	12.6	63.0	21	13	ADR67642	Adr67642 Human ret
45	12.6	63.0	21	13	ADS99597	Ads99597 Small int

ALIGNMENTS

RESULT 1

ADZ11151
ID ADZ11151 standard; DNA; 20 BP.

AC ADZ11151;

XX 16-JUN-2005 (first entry)

XX Human STAT3-specific antisense oligonucleotide - SEQ ID 342.

XX antisense oligonucleotide; antisense therapy; inflammation;
XX antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

OS Homo sapiens.

XX US2005074879-A1. — instant app.

XX 07-APR-2005.

XX 06-FEB-2004; 2004US-00773678.

XX 06-APR-2000; 2000WO-US009054.

XX 11-JAN-2001; 2001US-00758881.

XX 14-NOV-2003; 2003US-00713139.

XX (KARR/) KARRAS J G.

XX Karas JG;

XX WPI; 2005-272408/28.

XX New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).

XX Claim 13; SEQ ID NO 342; 149pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to


```
RESULT 4
ADZ11150
ID ADZ11150 standard; DNA; 20 BP.
XX
AC ADZ11150;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human STAT3-specific antisense oligonucleotide - SEQ ID 341.
XX
DE antisense oligonucleotide; antisense therapy; inflammation;
KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
KW brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX
OS Homo sapiens.
XX
PN US2005074879-A1.
XX
PD 07-APR-2005.
XX
PF 06-FEB-2004; 2004US-00773678.
XX
PR 06-APR-2000; 2000WO-US009054.
PR 11-JAN-2001; 2001US-00758881.
PR 14-NOV-2003; 2003US-00713139.
XX
PA (KARR/) KARRAS J G.
XX
PI Karas JG;
XX
PI WPI; 2005-272408/28.
XX
DR New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
PS Example 19; SEQ ID NO 341; 149pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 95.0%; Score 19; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ACTCTTGCAGGAGCGGCT 20
Db 1 ACTCTTGCAGGAGCGGCT 19
RESULT 5
ADZ11152
ID ADZ11152 standard; DNA; 20 BP.
XX
AC ADZ11152;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human STAT3-specific antisense oligonucleotide - SEQ ID 343.
XX
DE antisense oligonucleotide; antisense therapy; inflammation;
KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
KW brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX
OS Homo sapiens.
XX
PN US2005074879-A1.
XX
PD 07-APR-2005.
XX
PF 06-FEB-2004; 2004US-00773678.
XX
PR 06-APR-2000; 2000WO-US009054.
PR 11-JAN-2001; 2001US-00758881.
PR 14-NOV-2003; 2003US-00713139.
XX
PA (KARR/) KARRAS J G.
XX
PI Karas JG;
XX
PI WPI; 2005-272408/28.
XX
DR New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
PS Example 19; SEQ ID NO 341; 149pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;
Query Match 95.0%; Score 19; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 ACTCTTGCAGGAGCGGCT 20
Db 1 ACTCTTGCAGGAGCGGCT 19
RESULT 6
ADZ11149
ID ADZ11149 standard; DNA; 20 BP.
XX
AC ADZ11149;
XX
DT 16-JUN-2005 (first entry)
XX
DE Human STAT3-specific antisense oligonucleotide - SEQ ID 340.
XX
DE antisense oligonucleotide; antisense therapy; inflammation;
KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
KW brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX
OS Homo sapiens.
XX
PN US2005074879-A1.
XX
PD 07-APR-2005.
XX
PF 06-FEB-2004; 2004US-00773678.
XX
PR 06-APR-2000; 2000WO-US009054.
PR 11-JAN-2001; 2001US-00758881.
PR 14-NOV-2003; 2003US-00713139.
XX
PA (KARR/) KARRAS J G.
XX
PI Karas JG;
XX
PI WPI; 2005-272408/28.
XX
DR New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
PS Example 19; SEQ ID NO 343; 149pp; English.
XX
CC The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
SQ Sequence 20 BP; 4 A; 5 C; 7 G; 4 T; 0 U; 0 Other;
Query Match 90.0%; Score 18; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACTCTTGCAGGAGCGG 18
Db 3 GACTCTTGCAGGAGCGG 20
```

```

PD 07-APR-2005.
XX
XX
XX 06-FEB-2004; 2004US-00773678.
XX
XX 06-APR-2000; 2000WO-US009054.
XX 11-JAN-2001; 2001US-00758881.
XX 14-NOV-2003; 2003US-00713139.
XX
XX (KARR/) KARRAS J G.
XX
XX Karras JG;
XX
XX WPI; 2005-272408/28.
XX
XX New antisenese compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
XX Example 19; SEQ ID NO 340; 149pp; English.
XX
XX The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 85.0%; Score 17; DB 14; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 TCTTGCAGGAAGCGCT 20
XX |||||
XX 1 TCTTGCAGGAAGCGCT 17
XX
XX Db
XX
XX RESULT 7
XX ADZ11153
XX ID ADZ11153 standard; DNA; 20 BP.
XX
XX AC ADZ11153;
XX
XX 16-JUN-2005 (first entry)
XX
XX Human STAT3-specific antisense oligonucleotide - SEQ ID 344.
XX
XX antisense oligonucleotide; antisense therapy; inflammation;
XX antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX
XX Homo sapiens.
XX
XX US2005074879-A1.
XX
XX 07-APR-2005.
XX
XX 06-FEB-2004; 2004US-00773678.
XX
XX 06-APR-2000; 2000WO-US009054.
XX 11-JAN-2001; 2001US-00758881.
XX 14-NOV-2003; 2003US-00713139.
XX
XX (KARR/) KARRAS J G.
XX
XX Karras JG;
XX
XX WPI; 2005-272408/28.
XX
XX New antisenese compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).
XX
XX Example 19; SEQ ID NO 340; 149pp; English.
XX
XX The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX
XX Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 85.0%; Score 17; DB 14; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 TCTTGCAGGAAGCGCT 20
XX |||||
XX 1 TCTTGCAGGAAGCGCT 17
XX
XX Db
XX
XX RESULT 8
XX ADW26449
XX ID ADW26449 standard; DNA; 20 BP.
XX
XX AC ADW26449;
XX
XX 10-MAR-2005 (first entry)
XX
XX EGFR inhibitor cancer treatment prognostic marker PCR primer, SEQ ID 201.
XX
XX prognosis; selectable marker; cancer; cytostatic; ovary tumor;
XX colon tumor; pancreatic cancer; non-small-cell lung cancer; breast tumor;
XX head & neck tumor; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX WO2004111273-A2.
XX
XX 23-DEC-2004.
XX
XX 28-MAY-2004; 2004WO-US017215.
XX
XX 30-MAY-2003; 2003US-0474908P.
XX
XX (GENO-) GENOMIC HEALTH INC.
XX
XX Agus D, Baker JB, Natale R, Shak S;
XX WPI; 2005-040123/04.
XX
XX Predicting if a subject responds to epidermal growth factor receptor
XX (EGFR) inhibitor treatment, useful for cancer patients, by determining
XX expression level of prognostic RNA transcripts of genes e.g. FUS, or its
XX expression product.
XX
XX Claim 41; SEQ ID NO 201; 77pp; English.
XX
XX The invention comprises a method for predicting the likelihood that a
XX subject will respond to cancer treatment with an epidermal growth factor
XX receptor (EGFR) inhibitor. The method involves determining the expression

```

CC level of one or more prognostic RNA transcripts or their expression
CC products in a biological sample comprising cancer cells obtained from the
CC patient. The method of the invention is useful for predicting whether a
CC patient is likely to respond well to treatment with an EGFR inhibitor,
CC especially patients having: ovarian cancer, colon cancer, pancreatic
CC cancer, non-small cell lung cancer, breast cancer, and head/neck cancer.
CC The present DNA sequence represents a PCR primer which is specific for a
CC prognostic marker of the invention.

XX SQ Sequence 20 BP; 5 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 80.0%; Score 16; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAAGCGGCT 20
Db 1 CTTGCAGGAAGCGGCT 16
|||||

RESULT 9
ADZ11154
ID ADZ11154 standard; DNA; 20 BP.

AC ADZ11154;

XX DT 16-JUN-2005 (first entry)

XX DE Human STAT3-specific antisense oligonucleotide - SEQ ID 345.

XX antisense oligonucleotide; antisense therapy; inflammation;
XX antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

XX OS Homo sapiens.

XX PN US2005074879-A1.

XX PD 07-APR-2005.

XX PF 06-FEB-2004; 2004US-00773678.

XX PR 06-APR-2000; 2000WO-US009054.

XX PR 11-JAN-2001; 2001US-00758881.

XX PR 14-NOV-2003; 2003US-00713139.

XX XX (KARR/) KARRAS J G.

XX PI Karras JG;

XX WPI; 2005-272408/28.

XX New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).

XX Example 19; SEQ ID NO 345; 149pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.

XX SQ Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAG 15
Db 6 GACTCTTGCAGGAAG 20
|||||

RESULT 10

ADZ11148
ID ADZ11148 standard; DNA; 20 BP.

XX AC ADZ11148;

XX DT 16-JUN-2005 (first entry)

XX DE Human STAT3-specific antisense oligonucleotide - SEQ ID 339.

XX antisense oligonucleotide; antisense therapy; inflammation;
XX antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.

XX OS Homo sapiens.

XX PN US2005074879-A1.

XX PD 07-APR-2005.

XX PF 06-FEB-2004; 2004US-00773678.

XX PR 06-APR-2000; 2000WO-US009054.

XX PR 11-JAN-2001; 2001US-00758881.

XX PR 14-NOV-2003; 2003US-00713139.

XX XX (KARR/) KARRAS J G.

XX PI Karras JG;

XX WPI; 2005-272408/28.

XX New antisense compound, useful for treating or preventing inflammatory
XX diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX lymphomas).

XX Example 19; SEQ ID NO 339; 149pp; English.

XX The invention comprises antisense oligonucleotides that are targeted to
XX nucleic acid molecules encoding human signal transducers and activators
XX of transcription 3 (STAT3). The antisense oligonucleotides of the
XX invention inhibit expression of human STAT3. The antisense
XX oligonucleotides of the invention are useful for treating and preventing
XX inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX and lymphomas). The present DNA sequence represents a human STAT3-
XX specific antisense oligonucleotide. NOTE: The present sequence has a
XX phosphorothioate backbone, 2'-MOE wings and a deoxy gap.

XX SQ Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 75.0%; Score 15; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20
Db 1 TTGCAGGAAGCGGCT 15
|||||

```
RESULT 11
AAT78506
ID AAT78506 standard; DNA; 29 BP.
XX
AC AAT78506;
XX
DT 10-MAR-1998 (first entry)
XX
DE Thiol-specific antioxidant gene sense primer EukTSA sen.
XX
KW Thiol-specific antioxidant; helminth; cestode; nematode; trematode;
KW anthelmintic; heartworm; infection; therapy; PCR; primer; ss.
XX
OS Synthetic.
OS Dirofilaria immitis.
XX
FN WO9729766-A1.
XX
PD 21-AUG-1997.
XX
PF 13-FEB-1997; 97WO-US002361.
XX
PR 15-FEB-1996; 96US-00602262.
XX
PA (HESK-) HESKA CORP.
XX
PI Klimowski L, Tripp CA;
XX
XX WPI; 1997-424754/39.
XX
XX Nucleic acid encoding thiol-specific antioxidant protein of helminth
PT larvae - useful for treatment or prevention of helminth infection,
PT specifically heartworm.
XX
PS Example 8; Page 68; 88pp; English.
XX
CC This oligonucleotide comprises sense PCR primer EukTSA sen that contains
CC a BamHI site. It was used with antisense primer EukTSA ant (see AAT78507)
CC to amplify the coding region of the Dirofilaria immitis thiol-specific
CC antioxidant (TSA) protein gene (see AAT78497). The 620-nucleotide PCR
CC product was subcloned into the pKB3poly shuttle vector, and a recombinant
CC racoon provirus capable of directing production of TSA in eukaryotic
CC host cells was produced. TSA (see AAW23715) can be used in the treatment
CC or prevention of heartworm
XX
SQ Sequence 29 BP; 6 A; 9 C; 8 G; 6 T; 0 U; 0 Other;
Query Match 72.0%; Score 14.4; DB 2; Length 29;
Best Local Similarity 93.8%; Pred. No. 4.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GACTCTTGCAGGAGC 16
DB 14 GACTCTTGTGGAAGC 29
| | | | | | | | | | | | | |
RESULT 12
AAC93168
ID AAC93168 standard; DNA; 20 BP.
XX
AC AAC93168;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human STAT3 phosphorothioate antisense oligonucleotide SEQ ID NO:19.
XX
KW Human; mouse; STAT3; phosphorothioate; antisense oligonucleotide;
KW modulation; signal transducer and activator of transcription;
KW DNA-binding protein; signal transduction; inhibition; apoptosis;
KW inflammatory disease; cancer; antinflammatory; antirheumatic;
KW cytosolic; immunostimulatory; rheumatoid arthritis; leukaemia; myeloma;
KW melanoma; lymphoma; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO200061602-A1.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009054.
XX
PR 08-APR-1999; 99US-00288461.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Karras JG;
XX
XX WPI; 2000-619223/59.
XX
XX New antisense compound for inhibiting the expression of signal transducer
PT and activator of transcription 3 (STAT3) in cells or tissues and treating
PT diseases or condition associated with STAT3, such as rheumatoid arthritis
PT and cancer.
XX
PS Example 2; Page 46; 104pp; English.
XX
CC The present invention describes an antisense compound (I), 8 to 30
CC nucleobases in length, that is targeted to a nucleic acid molecule
CC encoding STAT3 (Signal Transducer and Activator of Transcription) and
CC which inhibits the expression of it. (I) has antinflammatory,
CC antirheumatic, cytostatic and immunostimulatory activities. (I) is used
CC for inhibiting the expression of STAT3 in cells or tissues, treating an
CC animal having a disease or condition associated with a reduction in apoptosis,
CC having a disease or condition characterised by a reduction in apoptosis,
CC and inducing apoptosis in a cell. Diseases or conditions that are treated
CC are rheumatoid arthritis, cancer of the breast, prostate, brain, head
CC and/or neck, leukaemia, myeloma, melanoma or lymphoma. (I) can also be
CC used for diagnostic methods in detecting and determining the role of
CC STAT3 in various cell functions, physiological processes and conditions
CC for diagnosing the conditions associated with expression of STAT3.
CC (I) can be used alone or with other drugs as an immunostimulator. (I) is
CC used in sandwich and colourimetric assays, involving enzyme conjugation
CC and radiolabeling and is used in diagnostic kits. AAC93150 encodes human
CC STAT3 and AAC93231 encodes mouse STAT3 as given in the exemplification of
CC the present invention. AAC93151 to AAC93230 and AAC93232 to AAC93299
CC represent STAT3 phosphorothioate antisense oligonucleotides, and AAC93300
CC represents a mismatch control oligonucleotide which are used in example
CC from the present invention
XX
SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;
Query Match 70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GACTCTTGCAGGAA 14
DB 7 GACTCTTGCAGGAA 20
| | | | | | | | | | | |
RESULT 13
AAS96785
ID AAS96785 standard; DNA; 20 BP.
XX
AC AAS96785;
XX
DT 26-FEB-2002 (first entry)
XX
DE Human STAT3 antisense phosphorothioate oligodeoxynucleotide #18.
XX
KW STAT3; human; signal transducer and activator of transcription; ss; STAT;
KW antisense gene therapy; Fas-mediated apoptosis; inflammatory disease;
KW autoimmune disease; rheumatoid arthritis; cancer; breast; prostate; head;
KW neck; brain; leukaemia; myeloma; melanoma; lymphoma; apoptosis;
KW antinflammatory; immunosuppressive; antirheumatic; antiarthritic;
KW cytostatic.
```

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XX OS Homo sapiens.
XX OS Synthetic.
XX PN US2001029250-A1.
XX PD 11-OCT-2001.
XX PF 11-JAN-2001; 2001US-00758881.
XX PR 08-APR-1999; 99US-00288461.
XX PR 06-APR-2000; 2000WO-US009054.
XX PA (KARR/) KARRAS J G.
XX PI Karras JG;
XX DR WPI; 2002-009991/01.
XX PT Novel antisense compound useful for treating and diagnosing inflammatory
XX PT diseases and cancers, is targeted to a nucleic acid molecule encoding
XX PT signal transducer and activator of transcription proteins.
XX PS Example 2; Page 13; 21pp; English.
XX CC The invention relates to antisense compounds targeted to a nucleic acid
XX CC molecule encoding a signal transducer and activator of transcription
XX CC (STAT) protein, specifically STAT3, where the antisense compounds inhibit
XX CC the expression of STAT3. The antisense sequences are useful for
XX CC inhibiting the expression of STAT3 in cells or tissues, inducing Fas-
XX CC mediated apoptosis in cells, and sensitising cells to apoptosis. They are
XX CC also useful for treating an animal having a disease or condition
XX CC associated with STAT3. These disorders include inflammatory or autoimmune
XX CC disease, particularly rheumatoid arthritis, cancers, such as those of the
XX CC breast, prostate, brain and head and neck and leukemias, myelomas,
XX CC melanomas and lymphomas. Also treatable are human diseases or conditions
XX CC characterised by a reduction in apoptosis or an insensitivity to
XX CC apoptotic signals. The sequences of the invention can be used in clinical
XX CC research, for detecting and determining the role of STAT3 in various cell
XX CC functions and physiological processes and for diagnosing conditions
XX CC associated with the expression of STAT3. The sequences represent cDNA
XX CC encoding human STAT3 and human STAT3 oligonucleotides
XX SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGAA 14
Db 7 GACTCTTCGAGAA 20

RESULT 14
ADZ10828
ID ADZ10828 standard; DNA; 20 BP.
XX AC ADZ10828;
XX DT 16-JUN-2005 (first entry)
XX DE Human STAT3-specific antisense oligonucleotide - SEQ ID 19.
XX KW antisense oligonucleotide; antisense therapy; inflammation;
XX KW antiinflammatory; rheumatoid arthritis; antiarthritic; antirheumatic;
XX KW cancer; cytostatic; breast tumor; prostate tumor; head & neck tumor;
XX KW brain tumor; multiple myeloma; melanoma; leukemia; lymphoma; STAT3; ss;
XX KW phosphorothioate; 2'-O-methoxyethyl; 2'-MOE wing.
XX OS Homo sapiens.
XX PN US2005074879-A1.

Query Match 70.0%; Score 14; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGAA 14
Db 7 GACTCTTCGAGAA 20

RESULT 15
AAC96250
ID AAC96250 standard; DNA; 25 BP.
XX AC AAC96250;
XX DT 26-FEB-2001 (first entry)
XX DE HLA DPA1 gene PCR primer #7.
XX KW DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO2000065088-A2.
XX DT 02-NOV-2000.
XX PF 20-APR-2000; 2000WO-EP003636.
XX PR 26-APR-1999; 99EP-00303215.
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX PI Ulfendahl P, Wong K;
XX DR WPI; 2000-679677/66.

XX 07-APR-2005.
XX 06-FEB-2004; 2004US-00773678.
XX 06-APR-2000; 2000WO-US009054.
XX 11-JAN-2001; 2001US-00758881.
XX 14-NOV-2003; 2003US-00713139.
XX PA (KARR/) KARRAS J G.
XX PI Karras JG;
XX DR WPI; 2005-272408/28.
XX PT New antisense compound, useful for treating or preventing inflammatory
XX PT diseases (e.g. rheumatoid arthritis) and cancers (breast, prostate, head
XX PT and neck, and brain cancer, myelomas, melanomas, leukemias, and
XX PT lymphomas).
XX PS Example 2; SEQ ID NO 19; 149pp; English.
XX CC The invention comprises antisense oligonucleotides that are targeted to
XX CC nucleic acid molecules encoding human signal transducers and activators
XX CC of transcription 3 (STAT3). The antisense oligonucleotides of the
XX CC invention inhibit expression of human STAT3. The antisense
XX CC oligonucleotides of the invention are useful for treating and preventing
XX CC inflammatory diseases (e.g. rheumatoid arthritis) and cancers (e.g.
XX CC breast, prostate, head and neck, brain, myelomas, melanomas, leukemias,
XX CC and lymphomas). The present DNA sequence represents a human STAT3-
XX CC specific antisense oligonucleotide. NOTE: The present sequence has a
XX CC phosphorothioate backbone, 2'-MOE wings and a deoxy gap.
XX SQ Sequence 20 BP; 6 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 70.0%; Score 14; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGAA 14
Db 7 GACTCTTCGAGAA 20

RESULT 15
AAC96250
ID AAC96250 standard; DNA; 25 BP.
XX AC AAC96250;
XX DT 26-FEB-2001 (first entry)
XX DE HLA DPA1 gene PCR primer #7.
XX KW DNA sequence analysis; sequencing; protein sequence; protein structure;
XX KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
XX KW human leukocyte antigen; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO2000065088-A2.
XX DT 02-NOV-2000.
XX PF 20-APR-2000; 2000WO-EP003636.
XX PR 26-APR-1999; 99EP-00303215.
XX PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX PI Ulfendahl P, Wong K;
XX DR WPI; 2000-679677/66.

```

XX Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
XX Claim 14; Page 48; 66pp; English.
XX
XX The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
XX
XX Sequence 25 BP; 4 A; 2 C; 6 G; 13 T; 0 U; 0 Other;
SQ
Query Match 69.0%; Score 13.8; DB 3; Length 25;
Best Local Similarity 88.2%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGCT 20
Db 9 TTTTGCAGGAAGCGGCT 25

RESULT 16
AAQ31029
ID AAQ31029 standard; RNA; 28 BP.
XX
XX AC AAQ31029;
XX
XX 25-MAR-2003 (revised)
DT 23-MAR-1993 (first entry)
XX
XX Circular antisense oligonucleotide GT to inhibit HSV-1.
DE
XX Closed oligonucleotide; immunomodulation; antiviral; antitumour;
KW exonuclease resistant; Herpes Simplex virus; cyclic; ss.
KW
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 1
FT /*tag= a
FT /note= "forms phosphodiester bond with 3'-OH of C at
FT position 28"
FT 28
FT misc_feature /*tag= b
FT /note= "forms phosphodiester bond with 5'-Phosphate group
FT of G at position 1"
FT
XX
XX W09219732-A1.
PN
XX
XX 12-NOV-1992.
PD
XX
XX 24-APR-1992; 92WO-FR000370.
PF
XX
XX 25-APR-1991; 91FR-00005114.
PR
XX
XX (GEST) GENSET.
PA
XX
XX Blumenfeld M, Brandys P, Dauriol L, Vasseur M;
XX
XX WPI; 1992-398859/48.
DR
XX
XX Cyclic sense or anti-sense closed oligo nucleotide(s) - useful for
XX therapeutic antiviral or anticancer agent, labelled diagnostic or
XX cosmetic applications, and natural immunomodulatory interferon inducer.
XX
XX Example 6; Page 50; 85pp; French.
XX

CC This is an example of a cyclic oligonucleotide of the invention. The
CC closed oligonucleotides are more resistant to exonuclease attack than
CC their linear counterparts. The nucleotides at position 1 and 28 are
CC brought into proximity for ligation by hybridisation to a complementary
CC linear oligonucleotide. The circularised form of oligonucleotide GT
CC inhibits HSV-1 multiplication (30% inhibition at 2microm and 65%
CC inhibition at 5microm). At these low concentrations, the circular
CC oligonucleotide has a higher inhibitory effect than its linear
CC counterpart. See AAQ31019-Q31028 for other examples. (Updated on 25-MAR-
CC 2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 28 BP; 3 A; 8 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 2; Length 28;
Best Local Similarity 88.2%; Pred. No. 7.9e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CTCTTGCGGAGCGGC 19
Db 12 CTCTTGCGGAGCGGC 28

RESULT 17
ADM14825/c
ID ADM14825 standard; DNA; 20 BP.
XX
XX ADM14825;
XX
XX 01-JUL-2004 (first entry)
DT
XX
XX Human mPGES-1 chimeric antisense oligonucleotide SEQ ID NO:1012.
DE
XX
XX chimeric; antisense oligonucleotide; phosphorothioate; human;
KW microsomal prostaglandin E2 synthase; mPGES-1; mPGES-1 inhibitor;
KW microsomal prostaglandin E2 synthase inhibitor; cytosolic; antidiabetic;
KW immunomodulator; cardiant; neuroprotective; antiinflammatory;
KW neuroprotective; nootropic; antiarthritic; vasotropic; ophthalmological;
KW immunomodulatory; cardiovascular; gene therapy; inflammation;
KW Alzheimer's disease; arthritis; diabetes; cancer; ischaemia;
KW reperfusion injury; ophthalmic disorder; immunological disorder;
KW cardiovascular disorder; neurological disorder; ss.
KW
XX Homo sapiens.
OS
XX Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= b
FT /mod_base= OTHER
FT /note= "phosphorothioate linkages and all cytidine
FT residues are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyls"
FT
XX
XX W02004028458-A2.
PN
XX
XX 08-APR-2004.
PD
XX
XX 25-SEP-2003; 2003WO-US030374.
PF
XX
XX 25-SEP-2002; 2002US-0413549P.
PR
XX
XX (PHAA) PHARMACIA CORP.
XX
XX Gierse JK;
PI
XX
XX WPI; 2004-305094/28.
DR

XX New antisense compound, having a sequence targeted to a nucleic acid
PT encoding mPGES-1, useful for preparing a composition for treating e.g.,
PT inflammation, Alzheimer's disease, arthritis, diabetes, cancer or
PT ischemia.
XX
PS Claim 4; SEQ ID NO 1012; 132pp; English.
XX
CC The present sequence represents a chimeric antisense oligonucleotide
CC targeted to human microsomal prostaglandin H2 synthase (mPGES-1). The
CC human mPGES-1 gene is located on chromosome 9, more specifically to
CC 9q34.3. The present invention also describes: (1) antisense compounds,
CC having a sequence comprising 8-30 bp targeted to a nucleic acid encoding
CC mPGES-1, which specifically hybridise with the nucleic acid mPGES-1 and
CC inhibits its expression; (2) a method of inhibiting the expression of
CC mPGES-1 in cells or tissues; and (3) a method of treating an animal
CC having a disease or condition associated with mPGES-1. mPGES-1 chimeric
CC antisense oligonucleotides and antisense compounds have cytostatic,
CC antidiabetic, immunomodulatory, cardiant, neuroprotective,
CC antiinflammatory, neuroprotective, nootropic, antiarthritic, vasotropic,
CC ophthalmological, immunomodulatory and cardiovascular activities, and can
CC be used as mPGES-1 inhibitors and in gene therapy. The antisense compound
CC can be used for preparing a composition for treating a disease or
CC condition associated with mPGES-1 e.g., inflammation, Alzheimer's
CC disease, arthritis, diabetes, cancer, ischaemia or reperfusion injury, or
CC ophthalmic, immunological, cardiovascular or neurological disorder.
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 12; Length 20;
Best Local Similarity 80.0%; Pred. No. 9.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAAGCGCT 20
||| ||||| ||||| |||||
Db 20 GATTCCTGCAGGAAGTGCT 1

RESULT 18
ADRA45889
ID ADRA45889 standard; DNA; 30 BP.
XX
AC ADRA45889;
XX
DT 18-NOV-2004 (first entry)
XX
DE PCR primer used to amplify the VPS28 mutant Vps28deltaN.
XX
KW viral budding; viral infectivity; enveloped virus; VPS28 protein;
KW TSG101 protein; human immunodeficiency virus; HIV-1; HIV-II;
KW Marburg virus; Ebola virus; small interfering RNA; siRNA;
KW viral infection; HIV infection; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO2004071462-A2.
XX
PD 26-AUG-2004.
XX
PF 12-FEB-2004; 2004WO-US004518.
XX
PR 12-FEB-2003; 2003US-0446909P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
PA (FUNC-) FUNCTIONAL GENETICS INC.
XX
PI Yu X, Liu B, Li L;
XX
DR WPI; 2004-615918/59.
XX

PT Reducing viral budding and infectivity from a human cell infected by an
PT enveloped virus (e.g. HIV) comprises contacting the cell with an agent
PT that modulates the interaction between a VPS28 protein and a TSG101

PT protein.

XX Example; SEQ ID NO 10; 71pp; English.

XX
CC The specification describes a method for reducing viral budding and
CC infectivity from a mammalian cell infected by an enveloped virus. The
CC method comprises contacting the mammalian cell with an agent that
CC modulates the interaction between a VPS28 protein and a TSG101 protein or
CC that regulates the expression of a VPS28 gene, or an antibody that binds
CC a VPS28 protein. The enveloped virus is selected from human
CC immunodeficiency virus (HIV) type-I, HIV-II, Marburg virus and Ebola
CC virus. The agent especially comprises a small interfering RNA (siRNA)
CC targeting the VPS28 gene. The method of the invention is useful for
CC treating viral infections, including HIV infections. It may also be used
CC for evaluating and screening drugs that can be used for treating viral
CC infections. PCR primers ADRA45888-ADRA45889 were used to amplify a VPS28
CC mutant. The amplified product was used to produce vectors for use in the
CC method of the invention.

XX Sequence 30 BP; 8 A; 5 C; 11 G; 6 T; 0 U; 0 Other;

Query Match 68.0%; Score 13.6; DB 13; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+04;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAAGCGCT 20
||| ||||| ||||| |||||
Db 8 GAGGCATGCAGGAAGCGTT 27

RESULT 19
ADRA45885
ID ADRA45885 standard; DNA; 30 BP.

XX ADRA45885;

XX 18-NOV-2004 (first entry)

DE PCR primer used to amplify a human VPS28-Flag fusion.

XX viral budding; viral infectivity; enveloped virus; VPS28 protein;
KW TSG101 protein; human immunodeficiency virus; HIV-1; HIV-II;
KW Marburg virus; Ebola virus; small interfering RNA; siRNA;
KW viral infection; HIV infection; PCR; primer; ss.

XX Synthetic.

XX WO2004071462-A2.

XX 26-AUG-2004.

XX 12-FEB-2004; 2004WO-US004518.

XX 12-FEB-2003; 2003US-0446909P.

XX (UYJO) UNIV JOHNS HOPKINS.
XX (FUNC-) FUNCTIONAL GENETICS INC.

XX Yu X, Liu B, Li L;

XX WPI; 2004-615918/59.

XX Reducing viral budding and infectivity from a human cell infected by an
XX enveloped virus (e.g. HIV) comprises contacting the cell with an agent
XX that modulates the interaction between a VPS28 protein and a TSG101
XX protein.

XX Example; SEQ ID NO 6; 71pp; English.

XX The specification describes a method for reducing viral budding and
XX infectivity from a mammalian cell infected by an enveloped virus. The
XX method comprises contacting the mammalian cell with an agent that
XX modulates the interaction between a VPS28 protein and a TSG101 protein or

CC that regulates the expression of a VPS28 gene, or an antibody that binds
CC a VPS28 protein. The enveloped virus is selected from human
CC immunodeficiency virus (HIV) type-I, HIV-II, Marburg virus and Ebola
CC virus. The agent especially comprises a small interfering RNA (siRNA)
CC targeting the VPS28 gene. The method of the invention is useful for
CC treating viral infections, including HIV infections. It may also be used
CC for evaluating and screening drugs that can be used for treating viral
CC infections. PCR primers ADR45884-ADR45885 were used to amplify a VPS28-
CC Flag fusion construct. The amplified product was used to produce vectors
CC for use in the method of the invention.

XX
XX
SQ Sequence 30 BP; 8 A; 5 C; 11 G; 6 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 13; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+04; 4; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GACTCTTGCAGGAAGCGGCT 20
||| ||||| ||||| |||||
Db 8 GAGGCATGCAGGAAGCGGTT 27

RESULT 20
ADR45887
ID ADR45887 standard; DNA; 30 BP.
XX
XX AC ADR45887;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE PCR primer used to amplify the VPS28 mutant Vps28deltaN1.
XX
XX KW viral budding; viral infectivity; enveloped virus; VPS28 protein;
XX TSG101 protein; human immunodeficiency virus; HIV-1; HIV-II;
XX Marburg virus; Ebola virus; small interfering RNA; siRNA;
XX viral infection; HIV infection; PCR; primer; ss.
XX
XX OS Synthetic.
XX
XX PN WO2004071462-A2.
XX
XX PD 26-AUG-2004.
XX
XX PF 12-FEB-2004; 2004WO-US004518.
XX
XX PR 12-FEB-2003; 2003US-0446909P.
XX
XX PA (UYJO) UNIV JOHNS HOPKINS.
XX (FUNC-) FUNCTIONAL GENETICS INC.
XX
XX PI Yu X, Liu B, Li L;
XX
XX DR WPI; 2004-615918/59.
XX
XX PT Reducing viral budding and infectivity from a human cell infected by an
XX enveloped virus (e.g. HIV) comprises contacting the cell with an agent
XX that modulates the interaction between a VPS28 protein and a TSG101
XX protein.
XX
XX PS Example; SEQ ID NO 8; 71pp; English.
XX
XX CC The specification describes a method for reducing viral budding and
XX infectivity from a mammalian cell infected by an enveloped virus. The
XX method comprises contacting the mammalian cell with an agent that
XX modulates the interaction between a VPS28 protein and a TSG101 protein or
XX that regulates the expression of a VPS28 gene, or an antibody that binds
XX a VPS28 protein. The enveloped virus is selected from human
XX immunodeficiency virus (HIV) type-I, HIV-II, Marburg virus and Ebola
XX virus. The agent especially comprises a small interfering RNA (siRNA)
XX targeting the VPS28 gene. The method of the invention is useful for
XX treating viral infections, including HIV infections. It may also be used
XX for evaluating and screening drugs that can be used for treating viral
XX infections. PCR primers ADR45886-ADR45887 were used to amplify a VPS28

CC mutant. The amplified product was used to produce vectors for use in the
CC method of the invention.

XX
XX SQ Sequence 30 BP; 8 A; 5 C; 11 G; 6 T; 0 U; 0 Other;
Query Match 68.0%; Score 13.6; DB 13; Length 30;
Best Local Similarity 80.0%; Pred. No. 1e+04; 4; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GACTCTTGCAGGAAGCGGCT 20
||| ||||| ||||| |||||
Db 8 GAGGCATGCAGGAAGCGGTT 27

RESULT 21
ABQ03332
ID ABQ03332 standard; DNA; 24 BP.
XX
XX AC ABQ03332;
XX
XX DT 11-JUN-2002 (first entry)
XX
XX DE Oligonucleotide adapter/capture probe 3323.
XX KW Oligonucleotide array; adapter sequence; probe; ss.
XX
XX OS Synthetic.
XX
XX PN WO200216649-A2.
XX
XX PD 28-FEB-2002.
XX
XX PF 27-AUG-2001; 2001WO-US026519.
XX
XX PR 25-AUG-2000; 2000US-0227948P.
XX PR 29-AUG-2000; 2000US-0228854P.
XX
XX PA (ILLU-) ILLUMINA INC.
XX
XX PI Gunderson K;
XX
XX DR WPI; 2002-292068/33.
XX
XX PT Array comprising adapter sequences useful for immobilizing or detecting a
XX target nucleic acid sequence, has different addresses comprising
XX different specific capture probes.
XX
XX PS Claim 1; Page 123; 261pp; English.
XX
XX CC The invention relates to an oligonucleotide array (I) comprising at least
XX 25 different addresses (adapter sequences) with each comprising a
XX different capture probe selected from a group consisting of the sequences
XX given in ABQ00010-ABQ13409. (I) is useful for immobilising a target
XX nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-
XX ABQ13409) to a target nucleic acid to form a modified target nucleic acid
XX and contacting the modified target nucleic acid with (I). The steps of
XX above method is useful for detecting a target nucleic acid, which further
XX comprises detecting the presence of the modified target nucleic acid
XX

XX SQ Sequence 24 BP; 6 A; 5 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 67.0%; Score 13.4; DB 6; Length 24;
Best Local Similarity 93.3%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 6 TTCGAGGAAGCGGCT 20
||| ||||| ||||| |||||
Db 6 TGGCAGGAAGCGGCT 20

RESULT 22
AA289440
ID AA289440 standard; DNA; 23 BP.

XX AAZ89440;
AC 15-JUN-2000 (first entry)
XX
XX Human type IV collagen alpha-3 chain primer #40.
DE
XX
XX Human; primer; immunogenic; alpha-3 chain; type IV collagen; therapy;
KW autoantibody; Goodpasture's syndrome; immunosuppression; ss.
XX
XX Homo sapiens.
XX WO200011475-A1.
XX
XX 02-MAR-2000.
XX
XX 20-AUG-1999; 99WO-SE001416.
XX
XX 21-AUG-1998; 98SE-00002788.
XX (WIES-) WIESLAB AB.
XX Wieslander J, Hellmark T;
XX WPI; 2000-246583/21.
XX
XX Novel immunogenic region recognized by autoantibodies from goodpasture's
PT patients for detecting their presence in circulating body fluid comprises
PT a non-collagenous approximately a3 chain domain of type IV collagen.
XX
XX Example; Page 13; 36pp; English.
XX
CC This invention describes a novel immunogenic region (I) comprising an
CC epitope of non-collagenous alpha-3 chain domain of type IV collagen which
CC has intact cysteine residues. The epitope is located in the amino
CC terminal end of alpha3 chain and is recognized by circulating
CC autoantibodies (A) from a Goodpasture's patient. The product of the
CC invention has immunosuppressive activity, blocks autoantibodies and kills
CC cells producing (A) with an epitope-toxin complex. (I) is used for in
CC vitro determination of (A) in a body fluid by contacting it with the
CC immunogenic polypeptide molecule or a recombinant nucleic acid and
CC determining antigen-antibody reaction by physical or chemical method. The
CC determination can also be done by contacting the body fluid with anti-
CC idiotypic antibodies and determining antigen-antibody reaction by
CC physical or chemical methods. (I) is also used in therapy for treating
CC Goodpasture's syndrome. AAZ89401-289440 represent primers used in the
CC isolation of the products of the invention
XX
SQ Sequence 23 BP; 4 A; 6 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 66.0%; Score 13.2; DB 3; Length 23;
Best Local Similarity 83.3%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 2 ACTCTTGACGAGGCGGC 19
Db 6 ACTTTTGACGAGCAGTCG 23
RESULT 23
ADH72962
ID ADH72962 standard; DNA; 25 BP.
XX
XX ADH72962;
AC
XX
XX 25-MAR-2004 (first entry)
DT
XX
DE M. tuberculosis capture oligonucleotide #70.
XX
KW ss; single nucleotide polymorphism; SNP detection; genotyping;
KW pathogen detection; pathogen identification.
XX
XX Mycobacterium tuberculosis.

XX US2003232341-A1.
XX 18-DEC-2003.
XX
XX 12-JUN-2002; 2002US-00170332.
XX
XX 12-JUN-2002; 2002US-00170332.
XX
XX (CASE/) CASEY W M.
XX (CHEN/) CHEN J.
XX (COLT/) COLTON H M.
XX (TAYL/) TAYLOR J D.
XX (WEIN/) WEINER M P.
XX
XX Casey WM, Chen J, Colton HM, Taylor JD, Weiner MP;
XX WPI; 2004-052156/05.
XX
XX Detecting single nucleotide polymorphisms in target nucleic acids, useful
PT for e.g. in genotyping or in pathogen detection and identification,
PT comprises detecting the labels in the hybridization products.
XX
XX Claim 1; SEQ ID NO 124; 60pp; English.
XX
XX The invention relates to a method of detecting a result from an
CC identification reaction to identify a selected nucleotide in a target
CC nucleic acid comprising detecting the label of the labelled detection
CC product in the hybridisation products, the presence of the label
CC indicating the identity of the selected nucleotide in the target nucleic
CC acid. The method is useful for rapid detection of single nucleotide
CC polymorphisms in a nucleic acid sample. These may be used for genotyping
CC (such as for disease mutation detection and for parentage determinations
CC in humans and other animals), pathogen detection and identification and
CC differential gene expression. The present sequence represents a
CC Mycobacterium tuberculosis capture oligonucleotide.
XX
SQ Sequence 25 BP; 5 A; 9 C; 5 G; 6 T; 0 U; 0 Other;
Query Match 66.0%; Score 13.2; DB 12; Length 25;
Best Local Similarity 83.3%; Pred. No. 1.5e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 3 CTCTTGCAGGAGCGGCT 20
Db 7 CTCTTGCAGGATACGGCT 24
RESULT 24
AAF46591/c
ID AAF46591 standard; DNA; 15 BP.
XX
XX AAF46591;
AC
XX
XX 30-MAR-2001 (first entry)
DT
XX
XX IGFBP3 oligonucleotide #11.
XX
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200078341-A1.
XX
XX 28-DEC-2000.
XX

DR WPI; 2001-041421/05.
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisenescence nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 7; Page 44; 201pp; English.
PS
XX The present invention relates to a method for ameliorating the effects of
XX skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAP45151 and AAP45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
XX Sequence 15 BP; 1 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
SQ Query Match 65.0%; Score 13; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 8 GCAGGAAGCGGCT 20
Db 15 GCAGGAAGCGGCT 3
RESULT 27
ID ADP14476 standard; DNA; 25 BP.
XX
XX ADP14476;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Renal cell carcinoma differentially expressed gene probe #881.
DE
XX ss: diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression; probe.
XX
XX Homo sapiens.
OS
XX
XX WO2004048933-A2.
PN
XX
XX 10-JUN-2004.
PD
XX
XX 21-NOV-2003; 2003WO-US037481.
XX
XX 21-NOV-2002; 2002US-0427982P.
PR
XX 03-APR-2003; 2003US-0459782P.
XX
XX (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREP/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
XX
XX Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
PI Sloni DK;
XX
XX WPI; 2004-460799/43.
DR

XX Diagnosing non-blood disease such as solid tumor, involves comparing
PT differential expression profile of specific genes in peripheral blood
PT sample of subject with reference expression profile of specific genes.
XX
XX Disclosure; SEQ ID NO 1212; 350pp; English.
PS
XX The invention relate to a method of diagnosing (M1) non-blood disease
CC such as solid tumor by providing peripheral blood sample of human having
CC non-blood disease, and comparing an expression profile of specific genes
CC in the peripheral blood sample to reference expression profile of the
CC genes, where each of the genes is differentially expressed in peripheral
CC blood mononuclear cells (PBMCs) of patients having the disease as
CC compared to PBMCs of normal humans. The method is useful for diagnosing
CC non-blood disease such as solid tumor. The solid tumor is chosen from
CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
CC sample is a whole blood sample (claimed). (M1) is useful for identifying
CC genes that are differentially expressed in peripheral blood samples
CC isolated at different stages of progression, development or treatment of
CC RCC and/or other solid tumors. This sequence corresponds to a probe to
CC detect a gene that is differentially expressed and detected by the method
CC of the invention.
XX
XX Sequence 25 BP; 8 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
SQ Query Match 65.0%; Score 13; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 TCTTGCAGGAAGC 16
Db 6 TCTTGCAGGAAGC 18
RESULT 28
ABS59220
ID ABS59220 standard; DNA; 26 BP.
XX
XX ABS59220;
AC
XX
XX 05-NOV-2002 (first entry)
DT
XX
XX Human G-protein coupled receptor, probe #123.
DE
XX
XX Human; G-protein coupled receptor; GPCR; cardiomyopathy; atherosclerosis;
KW diabetes; cell signal processing; metabolic pathway modulation; cancer;
KW adenocarcinoma; lymphoma; prostate cancer; uterus cancer; asthma;
KW immune response; neurodegenerative disorder; inflammatory disorder;
KW Crohn's disease; multiple sclerosis; Albright hereditary osteodystrophy;
KW probe; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200259313-A2.
PN
XX
XX 01-AUG-2002.
PD
XX
XX 18-DEC-2001; 2001WO-US049394.
XX
XX 18-DEC-2000; 2000US-0256635P.
PR
XX 21-DEC-2000; 2000US-0257876P.
PR
XX 04-JAN-2001; 2001US-0259743P.
PR
XX 10-JAN-2001; 2001US-0260718P.
PR
XX 12-JAN-2001; 2001US-0261498P.
PR
XX 24-JAN-2001; 2001US-0263689P.
PR
XX 08-FEB-2001; 2001US-0267454P.
PR
XX 22-FEB-2001; 2001US-0271021P.
PR
XX 14-MAR-2001; 2001US-0275946P.
PR
XX 23-MAR-2001; 2001US-0278150P.
PR
XX 18-APR-2001; 2001US-0284591P.
PR
XX 23-APR-2001; 2001US-0285718P.
PR
XX 19-JUN-2001; 2001US-0295327P.
PR

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PR 16-AUG-2001; 2001US-0312902P.
PA (CURA-) CURAGEN CORP.
XX
XX Li L, Ballinger RA, Padigaru M, Kekuda R, Colman SD, Spytek KA;
PI Casman SJ, Vernet CAM, Shenoy SG, Gusev V, Malyankar UM, Edinger S;
PI Gerlach V, Smithson G, Stone D, Sciore P, Macdougall JR, Gunther E;
PI Peyman JA, Ellerman K, Gangolli EA, Millet I;
XX WPI; 2002-599789/64.
XX
XX New G protein coupled receptor polypeptides and polynucleotides, useful
PT in gene therapy, particularly for treating or preventing cardiomyopathy,
PT atherosclerosis, diabetes, multiple sclerosis, Crohn's disease or cancer
PT in humans.
XX
XX Claim 1; Page 652; 685pp; English.
XX
XX The invention relates to novel isolated G-protein coupled receptor (GPCR)
CC polypeptides and polynucleotides. The GPCR polypeptide, GPCR nucleic acid
CC and antibody are useful for treating, preventing or alleviating a GPCR-
CC associated disorder or a pathological state in a subject, particularly a
CC human. In particular, the disorder is cardiomyopathy, atherosclerosis,
CC diabetes, or a disorder related to cell signal processing and metabolic
CC pathway modulation. The GPCR polypeptide and nucleic acid are also useful
CC for diagnosing the presence of or predisposition to a disease associated
CC and polypeptide are especially useful in therapeutic or prophylactic
CC applications for disorders associated with aberrant GPCR expression or
CC activity. The DNA encoding the protein is useful in gene therapy for
CC treating the above conditions. Furthermore, the nucleic acids and
CC polypeptides are useful in treating adenocarcinoma, lymphoma, prostate
CC cancer, uterus cancer, immune response, neurodegenerative disorders,
CC asthma, inflammatory disorders, Crohn's disease, multiple sclerosis or
CC Alzright hereditary osteodysplrophy. These are also useful in developing a
CC powerful assay system for functional analysis of various human disorders,
CC as well as in diagnostic applications. AB958747-AB959231 represent human
CC GPCR coding sequences, primers and probes of the invention
XX
XX Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match 65.0%; Score 13; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 TCTTGCAGGAAGC 16
Db 3 TCTTGCAGGAAGC 15
RESULT 29
ABT04530
ID ABT04530 standard; DNA; 26 BP.
XX
XX ABT04530;
XX
XX 25-SEP-2002 (first entry)
XX
XX Human G-protein coupled receptor probe SEQ ID NO: 473.
DE
XX Human; G-protein coupled receptor; GPCR; developmental disease;
XX immune disease; retinal disease; metabolic disorder; feeding disorder;
XX wasting disorder; infection; cancer; allergy; neurological disorder;
XX behavioural disorder; reproductive disorder; antidiabetic; cardiant;
XX antiatherosclerotic; probe; ss.
XX
XX Homo sapiens.
XX
XX WO200255558-A2.
XX
XX 18-JUL-2002.
XX
XX 18-DEC-2001; 2001WO-US049112.
XX

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XX 18-DEC-2000; 2000US-0256635P.
PR 18-DEC-2000; 2000US-0257876P.
PR 04-JAN-2001; 2001US-0259743P.
PR 10-JAN-2001; 2001US-0260718P.
PR 12-JAN-2001; 2001US-0261498P.
PR 24-JAN-2001; 2001US-0263689P.
PR 08-FEB-2001; 2001US-0267464P.
PR 22-FEB-2001; 2001US-0271021P.
PR 14-MAR-2001; 2001US-0275946P.
PR 23-MAR-2001; 2001US-0278150P.
PR 18-APR-2001; 2001US-0284591P.
PR 23-APR-2001; 2001US-0285718P.
PR 19-JUN-2001; 2001US-0299327P.
PR 16-AUG-2001; 2001US-0312902P.
XX
XX (CURA-) CURAGEN CORP.
PA
XX Padigaru M, Kekuda R, Li L, Ballinger RA, Casman SJ, Spytek KA;
PI Colman SD, Vernet CAM, Shenoy S, Gusev V, Malyankar UM, Edinger S;
PI Gerlach V, Smithson G, Stone D, Sciore P, Macdougall JR, Gunther E;
PI Peyman JA, Ellerman K, Millet I, Tchernev VT, Anderson DW, Wolenc A;
XX WPI; 2002-500840/53.
XX
XX New G-protein coupled receptor polypeptides, encoding nucleic acids and
PT immunospecific antibodies, useful for treating cardiomyopathy,
PT atherosclerosis, diabetes or disorder related to cell signal processing
PT and metabolic pathway modulation.
XX
XX Example 3; Page 457; 473pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC G-protein coupled receptors designated GPCRXX. These can be used in the
CC treatment of developmental diseases, immune diseases, retinal diseases,
CC metabolic disorders, feeding disorders, wasting disorders, infections,
CC cancer, allergies, neurological disorders, behavioural disorders and
CC reproductive disorders. The present sequence is a probe used to isolate a
CC coding sequence of the invention. The sequence is modified at the 5' end
CC by TET and at the 3' end by FAMRA
XX
XX Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;
SQ
Query Match 65.0%; Score 13; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 TCTTGCAGGAAGC 16
Db 3 TCTTGCAGGAAGC 15
RESULT 30
ABT05715
ID ABT05715 standard; DNA; 26 BP.
XX
XX ABT05715;
XX
XX 16-OCT-2002 (first entry)
XX
XX GPCR related probe SEQ ID No 168.
DE
XX Antidiabetic; cytostatic; anorectic; nootropic; neuroprotective; GPCRX;
XX antiparkinsonian; cardiant; antiarteriosclerotic; immunosuppressive;
XX hypotensive; haemostatic; antifertility; antidiastmatic; atherosclerosis;
XX anti-HIV; G-protein coupled receptor X; cardiomyopathy; antiinflammatory;
XX diabetes; metabolic disorder; diabetes; obesity; infectious disease;
XX anorexia; neurodegenerative disorder; Alzheimer's disease; dyslipidaemia;
XX Parkinson's disorder; immune disorder; haematopoietic disorder; obesity;
XX metabolic syndrome X; wasting disorder; cancer; hypertension; neoplasm;
XX congenital heart defect; aortic stenosis; subaortic stenosis; lymphoma;
XX transplantation; adrenoleukodystrophy; congenital adrenal hyperplasia;
XX prostate cancer; adenocarcinoma; uterus cancer; fertility; haemophilia;
XX

```

KW hypercoagulation; idiopathic thrombocytopenic purpura; immunodeficiency;
KW graft versus host disease; AIDS; bronchial asthma; Crohn's disease;
KW multiple sclerosis; chromosomal mapping; tissue typing; forensic biology;
KW gene therapy; transgenic animal; probe; ss.

XX Unidentified.

XX WO200246229-A2.

XX 13-JUN-2002.

XX 05-DEC-2001; 2001WO-US046530.

XX 05-DEC-2000; 2000US-0251459P.

PR 29-DEC-2000; 2000US-0259007P.

PR 04-DEC-2001; 2001US-00005041.

XX (CURA-) CURAGEN CORP.

XX Casman SJ, Padigar M, Burgess CE, Shimkets RA, Spytek KA;

PI Gilbert JA, Mayotte JE, Baumgartner JC, Mishra V, Vernet CAM;

PI Dickinson KS, Ballinger RA, Wolenc AR;

XX WPI; 2002-537559/57.

XX Example 2; Page 221; 264pp; English.

CC The invention relates to a novel isolated G-protein coupled receptor X
CC (GPCR) polypeptide. The isolated protein, its encoding polynucleotide
CC and the antibody of the isolated protein is useful for treating or
CC preventing a GPCR-associated disorder in a subject, preferably human.
CC where the disorder is cardiomyopathy, atherosclerosis or diabetes. The
CC isolated protein, its encoding polynucleotide and the antibody of the
CC isolated protein is useful for treating or preventing metabolic
CC disorders, diabetes, obesity, infectious disease, anorexia,
CC neurodegenerative disorder, Alzheimer's disease, Parkinson's disorder,
CC immune disorders, haematopoietic disorders, and various dyslipidaemias,
CC metabolic disturbances associated with obesity, the metabolic syndrome X,
CC wasting disorders associated with chronic diseases, and cancer. The
CC disorders also include cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, aortic stenosis, subaortic stenosis,
CC transplantation, adrenoleukodystrophy, congenital adrenal hyperplasia,
CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterus cancer,
CC fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic
CC purpura, immunodeficiencies, graft versus host disease, AIDS, bronchial
CC asthma, Crohn's disease, and multiple sclerosis. The isolated protein, its
CC encoding polynucleotide and the antibody of the isolated protein is
CC useful in screening assays, detection assays (e.g., chromosomal mapping,
CC tissue typing, forensic biology). The isolated polynucleotide is useful
CC in gene therapy, to express the isolated protein, to detect GPCR mRNA or
CC a genetic lesion in a GPCR gene, and to modulate GPCR activity. The
CC cell of the invention is useful for producing non-human transgenic
CC animals. This polynucleotide sequence represents a probe of a GPCR
CC protein of the invention

XX Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGC 16

Db 3 TCTTGCAGGAGC 15

|||||

RESULT 31

ADH31280

ID ADH31280 standard; DNA; 26 BP.

XX ADH31280;

XX 11-MAR-2004 (first entry)

XX Human G-protein coupled receptor (GPCR) cDNA probe #107.

XX Human; G-protein coupled receptor; GPCR; ss; GPCR; cardiomyopathy;
XX atherosclerosis; diabetes; obesity; infection; cancer;
XX Alzheimer's disease; Parkinson's disease; asthma; allergy; hypertension;
XX retinal disease; urinary retention; angina pectoris; Crohn's disease;
XX schizophrenia; manic depression; probe.

XX Homo sapiens.

XX OS

XX US2003232332-A1.

XX 18-DEC-2003.

XX 18-DEC-2001; 2001US-00024212.

XX 18-DEC-2000; 2000US-0256635P.

XX 21-DEC-2000; 2000US-0257876P.

XX 04-JAN-2001; 2001US-0259743P.

XX 10-JAN-2001; 2001US-0260718P.

XX 12-JAN-2001; 2001US-0261498P.

XX 24-JAN-2001; 2001US-0263689P.

XX 08-FEB-2001; 2001US-0267464P.

XX 22-FEB-2001; 2001US-0271021P.

XX 14-MAR-2001; 2001US-0275946P.

XX 23-MAR-2001; 2001US-0278150P.

XX 18-APR-2001; 2001US-0284591P.

XX 23-APR-2001; 2001US-0285718P.

XX 19-JUN-2001; 2001US-0299327P.

XX 16-AUG-2001; 2001US-0312902P.

XX (PADI) PADIGARU M.

XX (KEKU) KEKUDA R.

XX (LILL) LI L.

XX (BALL) BALLINGER R A.

XX (CASM) CASMAN S J.

XX (SPYT) SPYTEK K A.

XX (COLM) COLMAN S D.

XX (VERN) VERNET C A M.

XX (SHEN) SHENOY S G.

XX (GUSE) GUSEV V Y.

XX (MALY) MALYANKAR U M.

XX (EDIN) EDINGER S R.

XX (GERL) GERLACH V.

XX (SMIT) SMITHSON G.

XX (STON) STONE D J.

XX (SCIO) SCIORE P.

XX (MACD) MACDOUGALL J R.

XX (GUNT) GUNTHER E.

XX (PEYM) PEYMAN J A.

XX (ELLE) ELLERMAN K.

XX (MILL) MILLET I.

XX (TCHE) TCHERNEV V T.

XX (ANDE) ANDERSON D W.

XX (WOLE) WOLENC A R.

XX

XX Padigar M, Kekuda R, Li L, Ballinger RA, Casman SJ, Spytek KA;

XX Colman SD, Vernet CAM, Sheno S G, Gusev VY, Malyankar UM;

XX Edinger SR, Gerlach V, Smithson G, Stone DJ, Sciore P;

XX Macdougall JR, Gunther E, Peyman JA, Ellerman K, Millet I;

XX Tchernev VT, Anderson DW, Wolenc AR;

XX WPI; 2004-061267/06.

XX New G-protein coupled receptor (GPCR) polypeptides and nucleic acids,

XX useful for diagnosing, preventing or treating GPCR-associated disorders,

XX e.g. cardiomyopathy, atherosclerosis or diabetes, and in

XX pharmacogenomics.

XX PS Example 3; SEQ ID NO 472; 328pp; English.

XX CC The invention relates to human G-protein coupled receptor (GPCR)

XX CC polypeptides and the polynucleotides encoding them, designated GPCRXX. The

XX CC invention also relates to a vector comprising a GPCRXX nucleic acid, a

XX CC cell comprising the vector, an antibody that binds immunospecifically to

XX CC a GPCRXX polypeptide, methods for determining the presence or amount of

XX CC the polypeptide or the nucleic acid molecule in a sample, methods for

XX CC identifying an agent that binds to or modulates the expression or

XX CC activity of a polypeptide and a method for modulating the activity of the

XX CC polypeptide. The composition and methods are useful in diagnosing,

XX CC preventing or treating GPCRXX-associated disorders, such as

XX CC cardiomyopathy, atherosclerosis, diabetes, obesity, infections, cancer,

XX CC Alzheimer's disease, Parkinson's disease, asthma, allergies,

XX CC hypertension, retinal diseases, urinary retention, angina pectoris,

XX CC Crohn's disease, schizophrenia and manic depression. The nucleic acids

XX CC are further used as hybridisation probes, in chromosome mapping, tissue

XX CC typing, preventive medicine and pharmacogenomics. The polypeptides are

XX CC also useful as vaccines or as immunogens to produce antibodies. This

XX CC sequence represents a probe which hybridises to human GPCRXX cDNA of the

XX CC invention.

XX SQ Sequence 26 BP; 5 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 65.0%; Score 13; DB 12; Length 26;

Best Local Similarity 100.0%; Pred. No. 1.9e+04;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAAGC 16

Db |||||

3 TCTTGCAGGAAGC 15

RESULT 32

ADK98351/C

ID ADK98351 standard; DNA; 24 BP.

XX AC ADK98351;

XX DT 06-MAY-2004 (first entry)

XX XX Primer of the invention #4071.

DE human; single nucleotide polymorphism; SNP; ss; primer.

XX OS Synthetic.

XX PN JP2003259875-A.

XX PD 16-SEP-2003.

XX PF 08-MAR-2002; 2002JP-00064373.

XX PR 08-MAR-2002; 2002JP-00064373.

XX PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX DR WPI; 2004-093977/10.

XX PT Novel polynucleotide useful for PCR amplification along with two DNA

XX PT fragment from another set of sequences, or for detecting single

XX PT nucleotide polymorphism in human gene.

XX PS Claim 2; SEQ ID NO 7380; 2627pp; Japanese.

XX CC The present invention relates to a polynucleotide isolated from a human

XX CC gene and is useful for detecting a single nucleotide polymorphism in a

XX CC human gene or for diagnosing of disease. The invention enables the

XX CC detection of a single nucleotide polymorphism in a human gene. The

XX CC present sequence represents a primer of the invention.

XX SQ Sequence 24 BP; 5 A; 6 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 12; Length 24;

Best Local Similarity 87.5%; Pred. No. 2.4e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAAGC 16

Db |||||

19 GACTCTAGCAGGCAGC 4

RESULT 33

ACI12520

ID ACI12520 standard; DNA; 25 BP.

XX AC ACI12520;

XX DT 13-OCT-2003 (first entry)

XX DE Human microarray DNA oligonucleotide SEQ ID NO 12511.

XX KW EST; ss; probe; expressed sequence tag; microarray; gene expression;

XX KW genetic variation; biallelic marker; polymorphism; human;

XX KW cross-species comparison.

XX OS Homo sapiens.

XX PN US2003104410-A1.

XX PD 05-JUN-2003.

XX PF 15-MAR-2002; 2002US-00098263.

XX PR 16-MAR-2001; 2001US-0276759P.

XX PA (AFFY-) AFFYMETRIX INC.

XX PI Mittmann MP;

XX DR WPI; 2003-567953/53.

XX PT New array of nucleic acid probes, useful for in situ hybridization, in

XX PT Southern, Northern or dot-blot hybridization to identify or detect the

XX PT sequence or specific mutations of any gene.

XX PS Claim 1; SEQ ID NO 12511; 9pp; English.

XX CC The invention discloses a microarray comprising a plurality of nucleic

XX CC acid probes including one of 2,018,500 fully defined sequences, or its

XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.

XX CC Also disclosed is a method of gene expression analysis. The array is used

XX CC in monitoring gene expression levels by hybridisation to a DNA library,

XX CC in analysis of genetic variation or in hybridisation of tag-labelled

XX CC compounds. The nucleic acid probes are specifically designed for analysis

XX CC of at least one target sequence. The method of analysis comprises

XX CC hybridising at least one or more nucleic acids to at least two or more

XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid

XX CC probes are attached to a solid support. The analysis comprises monitoring

XX CC gene expression levels, identifying biallelic markers or polymorphisms,

XX CC or family members of a gene and a cross-species comparison. Each of the

XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid

XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-

XX CC blot hybridisation to identify or detect the sequence or specific

XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by

XX CC primer extensions or in screening cDNA or genomic libraries or subclones

XX CC for additional subclones containing segments of DNA that have been

XX CC isolated and previously sequenced. The sequence presented is one of the

XX CC nucleic acid probes incorporated in the microarray. Note: The sequence

XX CC data for this patent can also be obtained in electronic format directly

XX CC from USPTO at seqdata.uspto.gov/sequence.html

XX SQ Sequence 25 BP; 11 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 25;

Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAGC 16
|||||
DB 1 GACTCATGAGGAGC 16

RESULT 34
ACH63464
ID ACH63464 standard; DNA; 25 BP.
XX
AC ACH63464;
XX
DT 17-OCT-2003 (first entry)
XX
DE DNA target sequence #12600 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
PN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
PA (MITT/) MITTMANN M.
PI Mittmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analysing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 12600; 9pp; English.
XX
CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH5260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at segdata.uspto.gov/psipsiDentry.html
SQ Sequence 25 BP; 8 A; 5 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 25;

Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAGC 17
|||||
DB 9 ACTTTGCAGGAGC 24

RESULT 35
ACH51423
ID ACH51423 standard; DNA; 25 BP.
XX
AC ACH51423;
XX
DT 16-OCT-2003 (first entry)
XX
DE DNA target sequence #559 useful in array for genetic analyses.
XX
KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.
XX
OS Unidentified.
XX
PN US2003082596-A1.
XX
PD 01-MAY-2003.
XX
PF 08-AUG-2002; 2002US-00215112.
XX
PR 08-AUG-2001; 2001US-0311040P.
PA (MITT/) MITTMANN M.
PI Mittmann M;
XX
DR WPI; 2003-576608/54.
XX
PT New probe array useful e.g. for monitoring gene expression levels, for
PT analysing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.
XX
PS Claim 1; SEQ ID NO 559; 9pp; English.
XX
CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH5260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at segdata.uspto.gov/psipsiDentry.html
SQ Sequence 25 BP; 7 A; 4 C; 9 G; 5 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 25;

Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGC 19
||| ||| ||| ||| |||
Db 2 TCTTGAAGGAAGTGC 17

RESULT 36
ACH53400
ID ACH53400 standard; DNA; 25 BP.

XX AC ACH53400;

XX DT 16-OCT-2003 (first entry)

XX DE DNA target sequence #2536 useful in array for genetic analyses.

XX KW Gene expression analysis; array; hybridisation; genetic variation;
KW tag-labelled compound; gene family; in situ hybridisation;
KW library screening; Southern hybridisation; northern hybridisation;
KW dot-blot hybridisation; gene sequence; mutation detection;
KW target sequence; probe; PCR; primer; ss.

XX OS Unidentified.

XX PN US2003082596-A1.

XX PD 01-MAY-2003.

XX PF 08-AUG-2002; 2002US-00215112.

XX PR 08-AUG-2001; 2001US-0311040P.

XX PA (MITT/) MITTMANN M.

XX PI Mittmann M;

XX WPI; 2003-576608/54.

PT New probe array useful e.g. for monitoring gene expression levels, for
PT analyzing genetic variations, or for hybridizing tag-labeled compounds,
PT comprises multiple nucleic acid probes.

XX Claim 1; SEQ ID NO 2536; 9pp; English.

XX CC The present invention relates to nucleic acid sequences that are
CC complementary to particular genes, and can be used as probes for a
CC variety of analyses such as gene expression analysis. Each probe
CC comprises 9 or more consecutive nucleotides from at least one of 14936
CC nucleotide sequences defined in the patent, or their perfect sense match,
CC sense mismatch, antisense match or antisense mismatch oligonucleotides.
CC The probes may be used in an array comprising at least 10 distinct
CC nucleic acid probes. The array is useful in monitoring gene expression
CC levels by hybridisation to a DNA library, in analysing genetic
CC variations, and in hybridising tag-labelled compounds. The probes are
CC useful for identifying family members of a gene. The probes are also
CC useful in situ hybridisations, in screening cDNA or genomic libraries
CC (or derived subclones) for additional clones containing segments of DNA
CC that have been previously isolated and sequenced, in Southern, northern,
CC or dot-blot hybridisation of genomic DNA to identify or detect the
CC sequence of any gene or detect specific mutations in any gene, and in
CC mapping the 5' termini of mRNA molecules by primer extensions. The
CC nucleic acid sequences of the invention are also useful as PCR primers.
CC The invention provides a large collection of nucleic acid sequences
CC complementary to particular genes with a wide range of analytical uses.
CC ACH50865-ACH65260 represent the target sequences of the invention. Note:
CC The sequence data for this patent was obtained in electronic format
CC directly from the USPTO web site at seqdata.uspto.gov/paipsDIDEntry.html

XX SQ Sequence 25 BP; 6 A; 5 C; 5 G; 9 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 9; Length 25;

Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAGCG 17
||| ||| ||| ||| |||
Db 3 ACTTTTGAGGAGCG 18

RESULT 37

AAX22793
ID AAX22793 standard; DNA; 27 BP.

XX AC AAX22793;

XX DT 27-MAY-1999 (first entry)

XX DE PCR primer 84672.

XX KW Protein-enveloped polyribonucleic acid; viral RNA; bacteriophage RNA;
KW diagnostic; detection; assay; PCR primer; ss.

XX OS Synthetic.

XX PN DE19737442-A1.

XX PD 04-MAR-1999.

XX PF 22-AUG-1997; 97DE-01037442.

XX PR 22-AUG-1997; 97DE-01037442.

XX PA (OLF-) OLFERT LANDT TIB MOLBIOL SYNTHESLABOR.

XX PI Landt O;

XX WPI; 1999-168279/15.

PT Genetically modified RNA viruses or bacteriophages - useful as RNA
PT standards, positive controls, etc.

XX Example 5; Col 15; 12pp; German.

XX CC This invention describes protein-enveloped polyribonucleic acids
CC containing viral RNA or bacteriophage RNA, characterised in that the
CC natural nucleic acid sequence is varied. Also described is a method for
CC producing a protein-enveloped polyribonucleic acid. Protein-enveloped
CC polyribonucleic acids are useful as standards for diagnostic methods in
CC which the presence of a specific ribonucleic acid is detected, and are
CC useful as standard or competitor sequences for methods in which the
CC amount of a defined ribonucleic acid is determined. They are also useful
CC as positive controls for the detection of viral RNA, where the protein-
CC enveloped polyribonucleic acid is added directly to the assay sample and
CC is isolated in parallel with the viral RNA. They can monitor the
CC efficiency of processes for purifying nucleic acids or the efficiency of
CC the reverse transcription of ribonucleic acids, and are useful a
CC comparison substances in assays in which nucleic acids are detected by
CC hybridisation or in assays in which nucleic acids are detected after or
CC during nucleic acid amplification. They are useful as carriers for RNA
CC sequences having a functional property, and for mixtures of RNA sequences
CC from which individual RNA sequences can be selected

XX SQ Sequence 27 BP; 9 A; 6 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 64.0%; Score 12.8; DB 2; Length 27;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTTTCAGGAGCGCT 20
||| ||| ||| ||| |||
Db 8 CTTTCAGGAGCGCT 23

RESULT 38

ADCS1654
ID ADCS1654 standard; DNA; 27 BP.
XX AC ADCS1654;
XX DT 18-DEC-2003 (first entry)
XX DE 5' PCR primer to amplify human soluble transferrin receptor (stfr) cDNA.
XX KW Human; ss; PCR; primer; bioengineering process;
XX KW soluble type transferrin receptor; stfr; iron saturated transferrin;
XX KW transferrin receptor.
XX OS Homo sapiens.
XX PN JP2002369687-A.
XX PD 24-DEC-2002.
XX PF 18-MAY-2001; 2001JP-00148698.
XX PR 02-MAR-2001; 2001JP-00057780.
XX PA (EIKE) EIKEN KAGAKU KK.
XX DR WPI; 2003-472838/45.
XX PT A bioengineering safe, low cost and mass production process of a soluble
XX PT type transferrin receptor (stfr) used as markers of cancer and
XX PT hematopoietic function.
XX PS Example 3; Page 4; 9pp; Japanese.
XX CC The invention discloses a bioengineering process for the preparation of a
XX CC soluble type transferrin receptor (stfr). The process comprises the
XX CC preparation of a DNA encoding for an amino acid sequence of stfr,
XX CC preparation of a recombinant DNA by insertion of the DNA in a vector
XX CC (e.g. a vector containing a signal sequence, particularly an
XX CC immunoglobulin sequence), transformation of the recombinant DNA in host
XX CC cells, culture of the transformed host cells to produce stfr and
XX CC purification and collection of the produced stfr. Optionally, further
XX CC treatment of the collected stfr with an excess amount of iron saturated
XX CC transferrin, to give a complex, followed by purification of the complex,
XX CC particularly by an anionic ion exchange column, used for determination of
XX CC transferrin receptor in a living sample using the recombinant stfr as a
XX CC standard, can be carried out. The inventive process is safe, low cost and
XX CC is useful for mass production of stfr. The sequence presented is a PCR
XX CC primer which was used to amplify human stfr cDNA.
XX SQ Sequence 27 BP; 7 A; 7 C; 7 G; 6 T; 0 U; 0 Other;
Query Match 64.0%; Score 12.8; DB 10; Length 27;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 ACTCTGCGAGGACCG 17
|||||
Db 6 ACTCTGCGAGGACCG 21
RESULT 39
ABZ21923
ID ABZ21923 standard; DNA; 30 BP.
XX AC ABZ21923;
XX DT 28-MAR-2003 (first entry)
XX DE Mouse fusion protein dimer related PCR primer SEQ ID NO:14.
XX KW Mouse; prion protein dimer; fusion protein; vaccination; vaccine;
XX KW prion protein; virucide; immunostimulant; spongiform encephalopathy;
XX KW transmissible spongiform encephalopathy; PCR primer; ss.

XX Mus sp.
XX OS Synthetic.
XX PN EP1251138-A1.
XX PD 23-OCT-2002.
XX PF 19-APR-2001; 2001EP-00109707.
XX PR 19-APR-2001; 2001EP-00109707.
XX PA (SCHA/) SCHAETZL H.
XX PI Schaeztl H;
XX DR WPI; 2003-095100/09.
XX PT New prion protein dimer, useful as a vaccine against spongiform
XX PT encephalopathy.
XX PS Example 1; Page 6; 23pp; English.
XX CC The present invention describes a prion protein which is a homodimer or
XX CC heterodimer (I). Also described: (1) an antibody which specifically binds
XX CC the protein; (2) a DNA sequence encoding the protein; and (3) an
XX CC expression vector containing the DNA. (I) has virucide and
XX CC immunostimulant activities. The protein can be used for producing for
XX CC antibodies, and the protein, antibody, DNA and vector are useful for
XX CC preparing a vaccine for preventing or treating a transmissible spongiform
XX CC encephalopathy. There is no current vaccine for spongiform
XX CC encephalopathies. The present sequence represents a PCR primer used in
XX CC the generation of a fusion prion protein dimer in an example from the
XX CC present invention
XX SQ Sequence 30 BP; 9 A; 6 C; 10 G; 5 T; 0 U; 0 Other;
Query Match 64.0%; Score 12.8; DB 10; Length 30;
Best Local Similarity 87.5%; Pred. No. 2.4e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCTTGCAGGAGCGGC 19
|||||
Db 10 TCTTGCAGGAGCGGC 25
RESULT 40
ADM92376/C
ID ADM92376 standard; DNA; 20 BP.
XX AC ADM92376;
XX DT 01-JUL-2004 (first entry)
XX DE Pancreatic cancer related RT-PCR forward primer SEQ ID NO:13.
XX KW pancreatic cancer; diagnosis; pancreatic cancer-associated gene;
XX KW cytostatic; vaccine; gene therapy; human; reverse transcription; PCR;
XX KW primer; ss; semi-quantitative RT-PCR experiment.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO2004031412-A2.
XX PD 15-APR-2004.
XX PF 17-SEP-2003; 2003WO-JP011817.
XX PR 30-SEP-2002; 2002US-0414872P.
XX PR 28-FEB-2003; 2003US-0450889P.
XX PA (ONCO-) ONCOTHERAPY SCI INC.

(UUTY) UNIV TOKYO.

Nakamura Y, Katagiri T;
WPI; 2004-330205/30.

Diagnosing pancreatic cancer (PNC) comprises determining a level of
expression of a PNC-associated gene in a patient derived biological
sample.

Example 1; SEQ ID NO 13; 152bp; English.

The present invention describes a method for diagnosing pancreatic cancer
(PNC) or a predisposition to developing PNC in a subject. The method
comprises determining a level of expression of a PNC-associated gene in a
patient derived biological sample, where an increase or decrease of the
level compared to a normal control level of the gene indicates that the
subject suffers from or is at risk of developing PNC. Also described: (1)
a PNC reference expression profile, comprising a pattern of gene
expression of two or more genes, i.e. PNC 1-605 or PNC 850-866 and PNC
894-906; (2) a method of screening for a compound for treating or
preventing PNC or malignant PNC; (3) a kit comprising a detection reagent
which binds to two or more nucleic acid sequences, i.e. PNC 1-605 or PNC
850-866 and PNC 894-906 or the encoded polypeptides; (4) an array
comprising two or more nucleic acids which bind to one or more nucleic
acid sequences, i.e. PNC 1-605 or PNC 850-866 and PNC 894-906; (5) a
method of treating or preventing PNC in a subject; (6) a composition, for
treating or preventing PNC, comprising a pharmaceutical amount of: (a) an
antisense polynucleotide or small interfering RNA against a
polynucleotide, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-
933; (b) an antibody or antibody fragment that binds to a protein encoded
by any one gene, i.e. PNC 1-259, PNC 606-640 and PNC 682-741 or PNC 850-
933; or (c) the compound obtained by the method of (2) as an active
ingredient and a pharmaceutical carrier; and (7) a method of predicting
recurrence of PNC. The compounds have cytostatic activity, and can be
used in vaccines and in gene therapy. The method is useful in diagnosing
PNC or a predisposition to developing PNC in a subject. The methods,
compounds and compositions are useful in treating or preventing PNC. The
polypeptides are useful as vaccines against PNC. The present sequence
represents a reverse transcription (RT) PCR primer used in semi-
quantitative RT-PCR experiments related to the diagnosis of PNC, which is
used in an example from the present invention.

Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

```
Query Match          63.0%; Score 12.6; DB 12; Length 20;
Best Local Similarity 78.9%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 2 ACTCTTGCAGGAAGCGGCT 20
||| ||| ||| ||| ||| |||
Db 20 AATCTCCCAGGAAGCTGCT 2

Search completed: December 3, 2005, 13:29:58
Job time : 479 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:03:26 ; Search time 3651 Seconds
(without alignments)
256.297 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactcttgacgaagcgctg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 52094

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hic:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gsl1:*
10: gb_gsl2:*
11: gb_gsl3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11.4	57.0	25	6	CB412589 ScaE_0880
2	11.4	57.0	28	6	CB412564 ScaE_0852
3	11	55.0	30	10	CZ477398 d10718-3p
C 4	10.8	54.0	30	2	BF209105 601872801
C 5	10.8	54.0	30	8	DN955287 it85c02.g
C 6	10.6	53.0	20	9	AZ314365 IM0031G07
C 7	10.6	53.0	24	11	TA273G07Q
C 8	10.6	53.0	26	9	AZ622081 IM0455E10
9	10.6	53.0	28	1	AA895705 vyl14d02.r
10	10.6	53.0	28	10	CL663977 PRI0145d
11	10.6	53.0	29	1	AL045592 DKFZp434N
12	10.6	53.0	30	1	AL045336 DKFZp434A
13	10.6	53.0	30	1	AL045352 DKFZp434B
14	10.6	53.0	30	1	AL045477 DKFZp434H
15	10.6	53.0	30	1	AL045487 DKFZp434I
C 16	10.4	52.0	18	1	AJ650912 AJ650912
17	10.4	52.0	23	11	TA278H12P
18	10.4	52.0	24	9	AZ468735 IM0281114
C 19	10.4	52.0	28	1	AI429345 mn95c09.x
C 20	10.4	52.0	29	9	AZ472735 IM0288G08
21	10.4	52.0	29	9	AZ771858 IM0574P16
22	10.4	52.0	29	9	BH849150 SALK_0693

C 23	10.4	52.0	29	10	CZ442916	CZ442916 IB3F03.f
24	10.4	52.0	30	3	BM400275	BM400275 5009-0-70
C 25	10.2	51.0	19	6	CD532073	CD532073 L3104 Ara
C 26	10.2	51.0	20	9	AZ637794	AZ637794 IM0497D20
27	10.2	51.0	22	1	AA915121	AA915121 v203g03.r
28	10.2	51.0	27	8	DL8733	DL8733 MUGSO1795
29	10.2	51.0	27	10	CZ475704	CZ475704 d07387-5p
C 30	10.2	51.0	29	9	BZ595262	BZ595262 SALK_0863
31	10	50.0	27	9	AZ506426	AZ506426 IM0347M04
32	10	50.0	29	10	CZ467258	CZ467258 c01566-5p
33	10	50.0	29	11	TA36810P	AL453638 T. brucei
34	10	50.0	30	10	CZ471369	CZ471369 d00081-3p
35	9.8	49.0	22	1	AA912871	AA912871 ol27a02.s
C 36	9.8	49.0	27	9	AZ660103	AZ660103 IM0538801
C 37	9.8	49.0	28	1	AA633771	AA633771 ac27e01.s
38	9.8	49.0	28	1	AI005184	AI005184 ou60b01.x
C 39	9.8	49.0	28	1	AA192663	AA192663 zq03f12.s
C 40	9.8	49.0	29	10	AJ594066	AJ594066 Arabidops
41	9.8	49.0	30	10	CZ475056	CZ475056 d06331-3p
C 42	9.8	49.0	30	11	TA285E07Q	AL485454 T. brucei
C 43	9.6	48.0	20	9	AZ336487	AZ336487 IM0066J13
C 44	9.6	48.0	23	11	TA201E03Q	AL477466 T. brucei
45	9.6	48.0	25	8	L32049	L32049 HUMXP428A H

ALIGNMENTS

RESULT 1
CB412589
LOCUS
DEFINITION
ScaE_0880 Bay scallop Uni-ZAP XR Expression Library Argopecten
irradians cDNA 5' similar to Argopecten irradians cDNA library,
unknown, mRNA sequence.
ACCESSION
CB412589
VERSION
CB412589.1 GI:56934150
KEYWORDS
EST.
SOURCE
Argopecten irradians
ORGANISM
Argopecten irradians
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
Pectinoidea; Pectinidae; Argopecten.
REFERENCE
1 (bases 1 to 25)
Song, L., Xu, W., Li, H., Wu, L., Xiang, J. and Guo, X.
The construction and EST analysis of cDNA library from bay scallop
Argopecten irradians
Unpublished (2003)
JOURNAL
COMMENT
Contact: Longtao Wu
Experimental Marine Biology Laboratory (EMBL)
Institute of Oceanology, Chinese Academy of Science (IOCAS)
7 Nanhai Road, Qingdao, Shandong 266071, P. R. China
Tel: +86-0532-2898552
Email: lehong@ms.gdio.ac.cn
Seq primer: M13 Forward

FEATURES

source
1..25
/organism="Argopecten irradians"
/mol_type="mRNA"
/db_xref="taxon:31199"
/sex="hermaphrodite"
/tissue_type="whole body"
/clone_stage="maturation phase"
/clone_lib="Bay scallop Uni-ZAP XR Expression Library"
/note="Organ: whole body; Vector: pBluescript (+/-);
Site 1: XhoI; Site 2: EcoRI; Using Stratagene's Uni-ZAP XR
cDNA synthesis kit, we constructed a cDNA library of Bay
scallop. 4975 ESTs were gained."

ORIGIN

Query Match 57.0%; Score 11.4; DB 6; Length 25;
Best Local Similarity 92.3%; Pred. No. 8.4e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QC 7 TGCAGGAGCGGC 19

```

Db      8 TGCAGGAATCGGC 20
|||||
RESULT 2
CB412564          28 bp  mRNA  linear  EST 01-JAN-2005
LOCUS             Scae 0852 Bay scallop Uni-ZAP XR Expression Library Argopecten
DEFINITION        irradians cDNA 5' similar to Argopecten irradians cDNA library,
                  unknown, mRNA sequence.
ACCESSION         CB412564
VERSION           CB412564.1  GI:56934125
KEYWORDS          EST.
SOURCE            Argopecten irradians
ORGANISM          Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
                  Pectinoidea; Pectinidae; Argopecten.
REFERENCE         Song,L., Xu,W., Li,H., Wu,L., Xiang,J. and Guo,X.
AUTHORS           The construction and EST analysis of cDNA library from bay scallop
TITLE             Argopecten irradians
JOURNAL           Unpublished (2003)
COMMENT           Contact: Longtao Wu
                  Experimental Marine Biology Laboratory(EMBL)
                  Institute of Oceanology, Chinese Academy of Science (IOCAS)
                  7 Nanhai Road, Qingdao, Shandong 266071, P. R. China
                  Tel: +86-0532-2898352
                  Email: lshsong@ms.gdio.ac.cn
                  Seq primer: M13 Forward.
FEATURES          source
                  1..28
                  /organism="Argopecten irradians"
                  /mol_type="mRNA"
                  /db_xref="taxon:31199"
                  /sex="hermaphrodite"
                  /tissue_type="whole body"
                  /dev_stage="maturation phase"
                  /clone_lib="Bay scallop Uni-ZAP XR Expression Library"
                  /note="Organ: whole body; Vector: pBluescript(+/-);
                  Site_1: XhoI; Site_2: EcoRI; Using Stratagene's Uni-ZAP XR
                  cDNA synthesis Kit, we constructed a cDNA library of Bay
                  scallop. 4975 ESTs were gained."
ORIGIN
Query Match      57.0%; Score 11.4; DB 6; Length 28;
Best Local Similarity 92.3%; Pred. No. 8.5e+05;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 TGCAGGAATCGGC 19
|||||
Db      8 TGCAGGAATCGGC 20
|||||

RESULT 3
C2477398          30 bp  DNA  linear  GSS 29-APR-2005
LOCUS             dl0718-3prime Exelixis P element XP insertions Drosophila
DEFINITION        melanogaster genomic sequence recovered from 3' end of P element,
                  genomic survey sequence.
ACCESSION         C2477398
VERSION           C2477398.1  GI:62972730
KEYWORDS          GSS.
SOURCE            Drosophila melanogaster (fruit fly)
ORGANISM          Drosophila melanogaster
                  Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                  Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                  Ephydroidea; Drosophilidae; Drosophila.
REFERENCE         1 (bases 1 to 30)
                  Tibbault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
                  Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
                  Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
                  Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
                  Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,

Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
14981521
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element.
The P element insertion position is 1 in the 30 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon insertion site.
FEATURES          Location/Qualifiers
                  1..30
                  /organism="Drosophila melanogaster"
                  /mol_type="genomic DNA"
                  /strain="isogenic w- strain"
                  /db_xref="taxon:7227"
                  /clone_lib="Exelixis P element XP insertions"
                  /note="Vector: P element XP (GenBank accession number
                  AY515149); An isogenic w- Drosophila melanogaster strain
                  was mutagenized by remobilization of transposable
                  elements. For the P element XP, we selected an easily
                  mobilized ammunition element among inserts hopped onto the
                  Binsinsky balancer. New insertions were collected in vias
                  from dysgenic females using the standard chromosomal
                  source of transposase, delta2-3. All lines were mapped to
                  a chromosome by standard genetic methods, examined for
                  homozygous viability and used for recovery of flanking
                  genomic sequence by inverse PCR."
ORIGIN
Query Match      55.0%; Score 11; DB 10; Length 30;
Best Local Similarity 73.7%; Pred. No. 1.4e+06;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      2 ACTCTTCAGGAGCGGCT 20
|||||
Db      12 ACTCAGGAGGAAACCGCCT 30
|||||

RESULT 4
BF209105/c        30 bp  mRNA  linear  EST 06-NOV-2000
LOCUS             BF209105
DEFINITION        601872801F1 NIH_MGC_54 Homo sapiens cDNA clone IMAGE:4096776 5',
                  mRNA sequence.
ACCESSION         BF209105
VERSION           BF209105.1  GI:11102795
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                  Hominidae; Homo.
REFERENCE         1 (bases 1 to 30)
                  NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS           National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE             Unpublished (1999)
JOURNAL           Contact: Robert Strausberg, Ph.D.
COMMENT           Email: cgabs-x@mail.nih.gov
                  Tissue procurement: ATCC
                  cDNA Library Preparation: CLONETECH Laboratories, Inc.
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                  DNA sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be

```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW961 row: a column: 01
High quality sequence stop: 30.

FEATURES
source

1. 30
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4096776"
/tissue_type="from chronic myelogenous leukemia"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_54"

/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site 1: SfiI (ggcgctcgccg); Site 2: SfiI
(ggcattatggcc); Double-stranded cDNA was prepared from
cell line RNA. 5' and 3' adaptors were used in cloning as
follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and
3' adaptor sequence:
5'-ATCTAGAGCGCGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."

ORIGIN

Query Match 54.0%; Score 10.8; DB 2; Length 30;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTTGCAGGAAGCGG 18
Db 18 CTTGCAGGAATGCGG 5
|||||

RESULT 5

LOCUS DN955287/c 30 bp mRNA linear EST 04-MAY-2005
DEFINITION it85c02.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
sequence.
ACCESSION DN955287
VERSION DN955287.1 GI:63027425
KEYWORDS EST.
SOURCE Gnetum gnemon
ORGANISM Gnetum gnemon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales; Gnetales.

REFERENCE 1 (bases 1 to 30)
AUTHORS Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P., Coruzzi,G. and Stevenson,D.
Expressed tag sequences from Gnetum female cone (NYBG)
Unpublished (2003)

TITLE Contact: W. Richard McCombie
JOURNAL Lita Annenberg Hazen Genome Sequencing Center
COMMENT Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874

Email: mcombie@cshl.org
Seq primer: -21M13UnivRev.

FEATURES

source

1. 30
Location/Qualifiers
/organism="Gnetum gnemon"
/mol_type="mRNA"
/db_xref="taxon:3382"
/sex="female"

/clone_lib="Gnetum female cone (NYBG)"
/note="Organ: mature, unfertilized reproductive strobili;
Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
Completed 02/11/02, submitted for sequencing 02/12/02.
Library: Stratagene ZAP Express cDNA Synthesis Kit. The

ORIGIN

Query Match 54.0%; Score 10.8; DB 8; Length 30;
Best Local Similarity 85.7%; Pred. No. 1.7e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ACTCTTGACGGAAG 15
Db 14 ACCCTTGACGAGTAG 1
|||||

RESULT 6

LOCUS AZ314365/c 20 bp DNA linear GSS 29-SEP-2000
DEFINITION LM0031G07F Mouse 10kb plasmid UUCG1M library Mus musculus genomic
clone UUCG1M0031G07 F, genomic survey sequence.

ACCESSION AZ314365
VERSION AZ314365.1 GI:10360181
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0031 row: G column: 07

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

FEATURES

source

1. 20
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0031G07"
/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 53.0%; Score 10.6; DB 9; Length 20;
Best Local Similarity 76.5%; Pred. No. 2e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGGCT 20
||| ||||| ||||| ||
Db 20 TCCTCCAGGAAGCAGGT 4

RESULT 7

TA273G07Q/c
LOCUS T. brucei sheared genomic DNA clone 273g07, linear GSS 13-DEC-2000
DEFINITION genomic survey sequence.
ACCESSION AL487649
VERSION AL487649.1 GI:11852459
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 24)

REFERENCE

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre. The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk

AUTHORS

TITLE

JOURNAL
Constructd at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsavedetior.org

COMMENT

Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. .24
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="273g07"

FEATURES

source

ORIGIN

Query Match 53.0%; Score 10.6; DB 11; Length 24;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGCG 17
||| ||||| ||||| ||
Db 18 GATCATTCAGGAAGCG 2

RESULT 8

AZ622081/c
LOCUS 1M0455E10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0455E10 R, genomic survey sequence.
ACCESSION AZ622081
VERSION AZ622081.1 GI:11744271
KEYWORDS GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0455 row: E column: 10

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 26.

FEATURES

source

1. .26
Location/Qualifiers

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0455E10"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, TI-resistant, F."

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (GI|4732114|gb|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptored mouse DNA was annealed to

adaptored vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 53.0%; Score 10.6; DB 9; Length 26;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGGCT 20
||| ||||| ||||| ||
Db 24 TCTTGCAGTCAGCAGTT 8

RESULT 9

AA895705
LOCUS 28 bp mRNA linear EST 06-APR-1998
DEFINITION r1 Stratagene mouse macrophage (#937306) Mus musculus cDNA
clone IMAGE:1295427.5; similar to SW:DHAG.HUMAN P49189 ALDEHYDE
DEHYDROGENASE, E3 ISOZYME ;, mRNA sequence.
AA895705
ACCESSION


```

VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

FEATURES
source
1..28
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1295427"
/tissue_type="macrophage"
/dev_stage="WEHI-3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse macrophage (#937306)"
/note="Organ: blood; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAACTCGGACGAG 3' -3' adaptor sequence: 5' CTCAGTTTTTTTTTTTTTTT 3."

ORIGIN
Query Match 53.0%; Score 10.6; DB 1; Length 28;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTTCAGGAGCG 17
||| ||||| |||
Db 11 GACACTTGCTGCAGTG 27

RESULT 10
LOCUS
DEFINITION
CL663977 28 bp DNA linear GSS 09-JUL-2004
PRI0145d_E07 - PRI0145d_B21.1 (28) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL663977
GSS.
CL663977.1 GI:50153867
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 28)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
PUBMED
Contact: Sommer RJ

AA895705.1 GI:3032098
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Matra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lemon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:676475
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 3.
Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1295427"
/tissue_type="macrophage"
/dev_stage="WEHI-3 cell line"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse macrophage (#937306)"
/note="Organ: blood; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. WEHI-3 cell line. Average insert size: 1.5 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAACTCGGACGAG
3' -3' adaptor sequence: 5' CTCAGTTTTTTTTTTTTTTT 3."

ORIGIN
Query Match 53.0%; Score 10.6; DB 1; Length 28;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTTCAGGAGCG 17
||| ||||| |||
Db 11 GACACTTGCTGCAGTG 27

RESULT 10
LOCUS
DEFINITION
CL663977 28 bp DNA linear GSS 09-JUL-2004
PRI0145d_E07 - PRI0145d_B21.1 (28) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
CL663977
GSS.
CL663977.1 GI:50153867
Pristionchus pacificus
Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 28)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
14681447
PUBMED
Contact: Sommer RJ

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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..28
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pBpifos-5 Fosmid vector"

ORIGIN
Query Match 53.0%; Score 10.6; DB 10; Length 28;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTTCAGGAGCGG 18
||||| ||||| |||
Db 6 ACTCTAGCAGGGGGGG 22

RESULT 11
LOCUS
DEFINITION
AL045592 29 bp mRNA linear EST 06-JUL-2004
DKFZp434N025_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434N025 mRNA sequence.
AL045592
ACCESSION
VERSION
AL045592.1 GI:49682617
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 29)
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
EST (Duesterhoeft, et al.)
EST (Duesterhoeft, et al.)
Unpublished (1999)
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
Location/Qualifiers
1..29
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434N025"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN
Query Match 53.0%; Score 10.6; DB 1; Length 29;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTTCAGGAGCGG 18
||||| ||||| |||
Db 4 ACGCTGCAGGTACCGG 20

```


JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
source 1..30
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp341105"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="vector: pSport1; Site_1: Not1; Site_2: SalI"

ORIGIN
Query Match 53.0%; Score 10.6; DB 1; Length 30;
Best Local Similarity 76.5%; Pred. No. 2.1e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTGAGGAGCGG 18
|||||
Db 5 ACGCTGAGGTACGG 21

RESULT 16
LOCUS AJ650912 18 bp mRNA linear EST 07-JUL-2004
DEFINITION AJ650912 CSEQRAN19 Sus scrofa cDNA clone C0003276_L01, mRNA sequence.
ACCESSION AJ650912
VERSION AJ650912.1 GI:49327757
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 18)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Site1: EcoRI R. Site2: NotI 5'. Seq Primer M13F Normalised library constructed from pooled ovaries. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.ark-genomics.org.

FEATURES
source 1..18
Location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0003276_L01"
/tissue_type="ovary"
/clone_lib="CSEQRAN19"
/note="vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2: NotI; Single pass sequencing; Normalised library constructed from pooled ovaries"

ORIGIN
Query Match 52.0%; Score 10.4; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 2.5e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 GCAGGAAGCGG 19
|||||

Db 12 GCAGCAAGCGG 1
|||||

RESULT 17
LOCUS TA278H12P 23 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 278h12, forward sequence, genomic survey sequence.
ACCESSION AL485533
VERSION AL485533.1 GI:11851598
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 23)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="278h12"

ORIGIN
Query Match 52.0%; Score 10.4; DB 11; Length 23;
Best Local Similarity 91.7%; Pred. No. 2.6e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CTCTTGCGAGGAA 14
|||||
Db 10 CTATTGCGAGGAA 21
|||||

RESULT 18
LOCUS AZ468735 24 bp DNA linear GSS 04-OCT-2000
DEFINITION IM0281114R Mouse 10kb plasmid UUGCLM library Mus musculus genomic clone UUGCLM0281114 R, genomic survey sequence.
ACCESSION AZ468735
VERSION AZ468735.1 GI:10626776
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL plasmid inserts
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: cdunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0281 row: I column: 14
 Seq primer: CACACAGGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1. .24

FEATURES
 source
 1. .24
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGCIN0281114"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGCIN library"
 /note="Vector: pWD42nv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi14732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 10.4; DB 9; Length 24;
 Best Local Similarity 91.7%; Pred. No. 2.6e+06;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACTCTTGCGAG 12
 Db 7 GGCTCTTGCGAG 18

RESULT 19
 AI429345/c
 LOCUS
 DEFINITION
 m95c09.x1 Stratagene mouse lung 937302 Mus musculus cDNA clone
 IMAGE:551824 3', similar to TR:O15157 O15157 DOLICHOL MONOPHOSPHATE
 MANNOSE SYNTHASE ;, mRNA sequence.
 AI429345
 AI429345.1 GI:4275271
 EST.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 28)
 REFERENCE
 AUTHORS
 Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,

Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCam,R., Waterston,R. and Wilson,R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 COMMENT
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 This clone was previously sequenced on the 5' end only, this new data is from the 3' end
 Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand
 High quality sequence stop: 1.
 Location/Qualifiers
 1. .28

FEATURES
 source
 1. .28
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6 x CBA"
 /db_xref="taxon:10090"
 /clone="IMAGE:551824"
 /sex="female"
 /tissue_type="lung"
 /dev_stage="6-8 month old"
 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse lung 937302"
 /notes="Organ: lung; Vector: pBluescript SK-; Site 1: EcORI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. 6-8 month old female lung and 1.5 year old male lung were source of mRNA. Average insert size: 1.5 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGGACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match 52.0%; Score 10.4; DB 1; Length 28;
 Best Local Similarity 91.7%; Pred. No. 2.6e+06;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTTTCAGGAGC 16
 Db 28 CTTTCAGGAGC 17

RESULT 20
 AZ472735/c
 LOCUS
 DEFINITION
 1M0288G08F Mouse 10kb plasmid UUGCIN library Mus musculus genomic
 clone UUGCIN0288G08 F, genomic survey sequence.
 AZ472735
 AZ472735.1 GI:10630860
 GSS.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1 (bases 1 to 29)
 REFERENCE
 AUTHORS
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0288 row: G column: 08
 Seq primer: CGTTGTAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES

Location/Qualifiers
 1. .29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0288G08"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

1. .29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0574P16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 10.4; DB 9; Length 29;
 Best Local Similarity 91.7%; Pred. No. 2.6e+06;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 TGCAGGAAGCGG 18
 |||||
 Db 21 TGCAGGAAGGGG 10

RESULT 21

AZ771858
 LOCUS
 DEFINITION 1M0574P16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0574P16 F, genomic survey sequence.

ACCESSION AZ771858
 VERSION AZ771858.1 GI:12894560
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 29)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center

COMMENT
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0574 row: P column: 16
 Seq primer: CGTTGTAACGACGGCCAGT
 Class: plasmid ends
 High quality sequence stop: 29.

FEATURES

Location/Qualifiers
 1. .29
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0574P16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 52.0%; Score 10.4; DB 9; Length 29;
 Best Local Similarity 70.0%; Pred. No. 2.6e+06;
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GACTCTTGACGAGCGGCT 20
 |||||
 Db 6 GACCTGACGAGGGGCT 25

RESULT 22

BH849150
 LOCUS
 DEFINITION BH849150 29 bp DNA linear GSS 13-JUN-2002 SALK_069315.20.75.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_069315.20.75.x, genomic survey sequence.

ACCESSION BH849150
 VERSION BH849150.1 GI:21420021
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 29)

AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
 TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL Unpublished (2001)
 CONTACT: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGNAL)

COMMENT
 The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases from the 5' end of At2G40760.

Class: TDNA tagged.

Location/Qualifiers

1. .29

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Col-0"

/db_xref="taxon:3702"

/clone="SALK_069315.20.75.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

FEATURES source

ORIGIN

Query Match 52.0%; Score 10.4; DB 9; Length 29;
Best Local Similarity 70.0%; Pred. No. 2.6e+06;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAGCGGCT 20

||||| ||||| ||||| ||||| |||||

Db 8 GACTCGTACGGGAACACCT 27

RESULT 23

CZ442916/c

LOCUS

IBB3F03.fwd HIV-vector integration sites from well-expressed proviruses in human Jurkat T cells GSS 07-APR-2005

IBB3F03.fwd, genomic survey sequence.

CZ442916.1 GI:62379009

GSS.

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 29)

Lewinski, M.K., Bigsby, D., Shinn, P., Chen, H., Hoffmann, C.,

Hannenhalli, S., Verdin, E., Berry, C.C., Ecker, J.R. and Bushman, F.D.

Genome-wide analysis of chromosomal features repressing human

immunodeficiency virus transcription

J. Virol. 79 (11), 6610-6619 (2005)

15890899

Contact: Bushman FD

Department of Microbiology

University of Pennsylvania School of Medicine

402C Johnson Pavilion, 3610 Hamilton Walk, Philadelphia, PA

19104-6076, USA

Tel: 215 573 8732

Fax: 215 573 4856

Email: bushman@mail.med.upenn.edu

Class: PCR with specific primers.

Location/Qualifiers

1. .29

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="IBB3F03.fwd"

/cell_line="Jurkat"

/clone_lib="HIV-vector integration sites from

well-expressed proviruses in human Jurkat T cells"

/note="Vector: LTR-Tat-IRRES-GFP (pEV731); We have

FEATURES source

investigated regulatory sequences in noncoding human DNA that are associated with repression of an integrated human immunodeficiency virus type 1 (HIV-1) promoter. HIV-1 integration results in the formation of precise and homogeneous junctions between viral and host DNA, but integration takes place at many locations. Thus, the variation in HIV-1 gene expression at different integration sites reports the activity of regulatory sequences at nearby chromosomal positions. Negative regulation of HIV transcription is of particular interest because of its association with maintaining HIV in a latent state in cells from infected patients. To identify chromosomal regulators of HIV transcription, we infected Jurkat T cells with an HIV-based vector transducing green fluorescent protein (GFP) and separated cells into populations containing well-expressed (GFP-positive) or poorly expressed (GFP-negative) proviruses. We then determined the chromosomal locations of the two classes by sequencing 971 junctions between viral and cellular DNA. Possible effects of endogenous cellular transcription were characterized by transcriptional profiling. Low-level GFP expression correlated with integration in (i) gene deserts, (ii) centromeric heterochromatin, and (iii) very highly expressed cellular genes. These data provide a genome-wide picture of chromosomal features that repress transcription and suggest models for transcriptional latency in cells from HIV-infected patients."

ORIGIN

Query Match 52.0%; Score 10.4; DB 10; Length 29;
Best Local Similarity 70.0%; Pred. No. 2.6e+06;
Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GACTCTTCAGGAGCGGCT 20

||||| ||||| ||||| ||||| |||||

Db 23 GTCTTTTCTGGGAGCTGCT 4

RESULT 24

BM400275

LOCUS

5009-0-70-C02.t.1 Chilcoat/Turkewitz cDNA (large fraction)

Tetrahymena thermophila cDNA, mRNA sequence.

BM400275.1 GI:18200328

EST.

KEYWORDS

SOURCE

ORGANISM

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.

1 (bases 1 to 30)

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,

Frankel, J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

Location/Qualifiers

1. .30

/organism="Tetrahymena thermophila"

/mol_type="mRNA"

/strain="CU428.1"

/db_xref="taxon:5911"

/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"

/note="Vector: Bluescript2 SK+; Details on library

preparation can be found in Chilcoat and Turkewitz

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 52.0%; Score 10.4; DB 3; Length 30;
 Best Local Similarity 70.0%; Pred. No. 2.7e+06;
 Matches 14; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 GACTCTTCAGGAGCGGCT 20
 ||||| | ||||| ||
 Db 8 GACTCACGGGGGAGCGGCT 27

RESULT 25

CD532073/c
 LOCUS CD532073 19 bp mRNA linear EST 31-DEC-2003
 DEFINITION 13104 Arabidopsis Leaf Senescence Library Arabidopsis thaliana cDNA
 3', mRNA sequence.

ACCESSION CD532073
 VERSION CD532073.1 GI:40452085
 KEYWORDS EST.

SOURCE

ORGANISM Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 19)

Guo,Y., Cai,Z. and Gan,S.

Transcriptome of Arabidopsis leaf senescence

Plant Cell Environ. 27 (5), 521-549 (2004)

Contact: Susheng Gan

Department of Horticulture

Cornell University

119 Plant Science, Cornell University, Ithaca, NY 14853-5904, USA

Tel: 607 254 5418

Fax: 607 255 0599

Email: sg288@cornell.edu

Insert Length: 19 Std Error: 0.00

Seq primer: 17

POLYA=No.

FEATURES

source

Location/Qualifiers

1..19
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /ecotype="Landsberg erecta"
 /db_xref="taxon:3702"
 /tissue_type="Leaf"
 /dev_stage="Yellow Leaf With Greenish Base Area"
 /lab_host="E. coli"
 /clone_lib="Arabidopsis Leaf Senescence Library"
 /note="Organ: Rosette Leaf; Vector: pBluescript SKII+;
 Site 1: EcoRI; Site 2: EcoRI; Senescent rosette leaves #5
 and #6 (counted from the bottom) were harvested and
 immediately frozen in liquid N2. The leaves were visibly
 yellow excepted for the leaf base areas that were still
 greenish."

ORIGIN

Query Match 51.0%; Score 10.2; DB 6; Length 19;
 Best Local Similarity 80.0%; Pred. No. 3.1e+06;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 5 CTTGACGAGGCGC 19
 ||||| | ||||| ||
 Db 19 CGTGAAGGAGCAGC 5

RESULT 26

AZ637794/c
 LOCUS AZ637794 20 bp DNA linear GSS 13-DEC-2000
 DEFINITION 1M0497D20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 clone UUGC1M0497D20 F, genomic survey sequence.

ACCESSION AZ637794

VERSION AZ637794.1 GI:11759984

KEYWORDS GSS.

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
 Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0497 row: D column: 20

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1..20

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUGC1M0497D20"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"

/clone_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of PWD42 (G114732114|9B|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

ORIGIN

Query Match 51.0%; Score 10.2; DB 9; Length 20;
 Best Local Similarity 80.0%; Pred. No. 3.2e+06;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 GACTCTTCGACGAGAG 15
 ||||| | ||||| ||
 Db 16 GGCTCTTGGAGGAG 2

RESULT 27

AA915121

LOCUS

DEFINITION

AA915121

22 bp mRNA linear

EST 14-APR-1998

AA915121

22 bp mRNA linear

EST 14-APR-1998

AA915121

22 bp mRNA linear

EST 14-APR-1998

```

VERSION AA915121.1 GI:30545113
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 22)
TITLE Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HWMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HWMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouse@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:684972
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28m3 rev2 Et from Amersham
High quality sequence stop: 1.
FEATURES
source
1..22
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1314676"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_lib="Soares_mammary_gland_NbMWG"
/notes="Organ: mammary gland; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1:
Site 2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGGCGCGCGAATGGTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

ORIGIN
Query Match 51.0%; Score 10.2; DB 1; Length 22;
Best Local Similarity 80.0%; Pred. No. 3.2e+05;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAAG 15
| | | | |
Db 8 GATTCCTTCATGAAG 22

RESULT 28
D18733
LOCUS D18733
DEFINITION MUSG01795 Mouse 3'-directed Mus musculus cDNA clone md0789 3',
mRNA sequence.
ACCESSION D18733
VERSION D18733.1 GI:1100702
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

AA915121.1 GI:30545113
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 27)
TITLE Kawanoto,S., Okubo,K., Yoshii,J., Katsuki,M. and Matsubara,K.
Analysis of gene expression in mouse embryogenesis by 3'-directed
cDNA sequencing
JOURNAL Unpublished (1995)
COMMENT Contact: Shoko Kawanoto
Institute for Cellular and Molecular Biology
Osaka University
1-3, Yamadaoka, Suita, Osaka, 565, Japan
Email: shoko@next.imcb.osaka-u.ac.jp.
FEATURES
source
1..27
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="md0789"
/tissue_type="decidual tissue (day 6.5-8.5 of gestation)"
/clone_lib="Mouse 3'-directed"

ORIGIN
Query Match 51.0%; Score 10.2; DB 8; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.3e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCTTGCGAGGAGCGG 18
| | | | |
Db 3 TCTTGCGAGTCAGCTG 17

RESULT 29
CZ475704
LOCUS CZ475704
DEFINITION D07387-5prime Exelixis P element XP insertions Drosophila
melanogaster genomic Sequence recovered from 5' end of P element,
genomic survey sequence.
ACCESSION CZ475704 GI:62969731
VERSION CZ475704.1
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Drosophila melanogaster

REFERENCE
AUTHORS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 27)
TITLE Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,P.,
Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
JOURNAL Nat. Genet. 36 (3), 283-287 (2004)
PUBMED 14981521
COMMENT Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: RHoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element.
The P element insertion position is 20 in the 27 bases. This
insertion position refers to the first base of the 8 base target
recognition sequence.
Class: transposon insertion site.

```


FEATURES
source

Location/Qualifiers
1. .27
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis P element XP insertions"
/note="Vector: P element XP (GenBank accession number AY151149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized amputation element among inserts hopped onto the Binsincy balancer. New insertions were collected in vials from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

ORIGIN

Query Match 51.0%; Score 10.2; DB 10; Length 27;
Best Local Similarity 80.0%; Pred. No. 3.3e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTTGAGGAAGCGC 19

Db 13 CTCGAAGGAGAGGC 27

RESULT 30

BZ595262/c

LOCUS

DEFINITION BZ595262 29 bp DNA linear GSS 07-JAN-2003
SALK_086377.15.90.n Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_086377.15.90.n, genomic
survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 29)

REFERENCE

AUTHORS

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shinn, P., Zimmerman, J. and Ecker, J.R.

TITLE

JOURNAL

COMMENT

A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At4g25580.
Class: TDNA tagged.

Location/Qualifiers
1. .29
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="SALK_086377.15.90.n"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can

FEATURES

source

Location/Qualifiers
1. .29
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="SALK_086377.15.90.n"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can

ORIGIN

Query Match 51.0%; Score 10.2; DB 9; Length 29;
Best Local Similarity 80.0%; Pred. No. 3.3e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 4 TCTTGCGAGGAAGCGG 18
Db 18 TCTTGCGAGGAGCGG 4

RESULT 31

AZ506426

LOCUS

DEFINITION AZ506426 27 bp DNA linear GSS 05-OCT-2000
1M0347M04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0347M04 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 27)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0347 row: M column: 04
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES

source

Location/Qualifiers
1. .27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0347M04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptor DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into

be found at http://signal.salk.edu/tdna_protocols.html

chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

ORIGIN
Query Match          50.0%; Score 10; DB 9; Length 27;
Best Local Similarity 72.2%; Pred. No. 4.1e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACTCTTGCGAGGACGG 18
    |||||
Db 5 GCCTGTTGTAGGAGGGG 22

RESULT 32
CZ467258          29 bp DNA linear GSS 29-APR-2005
LOCUS
DEFINITION
col566-5prime Exelixis piggyBac PB insertions Drosophila
melanogaster genomic sequence recovered from 5' end of piggyBac,
genomic survey sequence.
ACCESSION
CZ467258
VERSION
CZ467258.1 GI:62961271
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 29)
REFERENCE
AUTHORS
Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
Ryner,L., Hartung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
Greer,K., Chaoutoni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
Swimmer,C., Kopczyński,C., Duyk,G., Winberg,M.L. and Margolis,J.
A complementary transposon tool kit for Drosophila melanogaster
using P and piggyBac
Nat. Genet. 36 (3), 283-287 (2004)
14981521
COMMENT
Contact: Roger A Hoskins
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
Tel: 510 486 4015
Fax: 510 486 6798
Email: Rhoskins@lbl.gov
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of
piggyBac element.
The piggyBac insertion position is 26 in the 29 bases. This
insertion position refers to the first base of the 4 base TTAA
target recognition sequence.
Class: transposon insertion site.
Location/Qualifiers
1. .29
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="isogenic w- strain"
/db_xref="taxon:7227"
/clone_lib="Exelixis piggyBac PB insertions"
/notes="Vector: piggyBac PB (GenBank accession number
AY515146); An isogenic w- Drosophila melanogaster strain
was mutagenized by remobilization of transposable
elements. We remobilized the PB element using
Hsp70:piggyBac transposase from a single ammunition
element on either the X or third chromosome. We induced
transposase expression by immersing bottles in a
circulating 370C water bath for a daily (days 3-10 after
egg-laying) 1-h heat shock. We outcrossed the resulting
dysgenic males to an isogenic w- strain. New insertions
were identified on the basis of a change in eye color
(third chromosome ammunition) or the appearance of w+ male
progeny (X chromosome ammunition). All lines were mapped

```

to a chromosome by standard genetic methods, examined for homozygous viability, and used for recovery of flanking genomic sequence by inverse PCR."

```

ORIGIN
Query Match          50.0%; Score 10; DB 10; Length 29;
Best Local Similarity 72.2%; Pred. No. 4.2e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CTCTTGCGAGGACGGCT 20
    |||||
Db 5 CTCTGGAACGGCGCGCT 22

RESULT 33
TA36B10P          29 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION
T. brucei sheared genomic DNA clone 36b10, forward sequence,
genomic survey sequence.
ACCESSION
AL453638
VERSION
AL453638.1 GI:11854781
KEYWORDS
SOURCE
Trypanosoma brucei
ORGANISM
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 29)
REFERENCE
AUTHORS
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submision
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. .29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="36b10"

FEATURES
source
1. .29
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="36b10"

ORIGIN
Query Match          50.0%; Score 10; DB 11; Length 29;
Best Local Similarity 72.2%; Pred. No. 4.2e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 CTCTTGCGAGGACGGCT 20
    |||||
Db 9 CTGCTGTCGAGGCGGAT 26

RESULT 34
CZ471369          30 bp DNA linear GSS 29-APR-2005
LOCUS
DEFINITION
d00081-3prime Exelixis P element XP insertions Drosophila
melanogaster genomic Sequence recovered from 3' end of P element,
genomic survey sequence.
ACCESSION
CZ471369
VERSION
CZ471369.1 GI:62965382

```


Fax: 801 585 7177
Email: ddum@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0538 row: B column: 01
Seq primer: CGTGTAAACGACGCCGACGT
Class: plasmid ends
High quality sequence stop: 27.
Location/Qualifiers

FEATURES
source

1..27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0538B01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

* ORIGIN

Query Match 49.0%; Score 9.8; DB 9; Length 27;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGC 19
|||||||
Db 19 TGCAGGAATTGCC 7

RESULT 37
AA633771/c
LOCUS
DEFINITION
ac27e01.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:857688 3' similar to SW:CYB_HUMAN P00156 CYTOCHROME B ;, mRNA sequence.
AA633771 28 bp mRNA linear EST 06-MAR-1998
IMAGE:857688 3' similar to SW:CYB_HUMAN P00156 CYTOCHROME B ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AA633771.1 GI:2556985
EST.
Homo sapiens (human)
Homo sapiens

REFERENCE
AUTHORS
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie, T., Waterston, R., and Wilson, R. WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 709 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:857688"
/sex="female"
/dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene ovary (#937217)"
/notes="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTGGCAGCAG 3' ~3' adaptor sequence: 5' CTCAGATTTTTTTTTTTT 3'"

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
Best Local Similarity 84.6%; Pred. No. 5.2e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 TGCAGGAAGCGGC 19
|||||||
Db 15 TGTAGGAAGAGGC 3

RESULT 38
AI005184
LOCUS
DEFINITION
ou60b01.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1632169 3' similar to TR:Q13162 Q13162 ANTIOXIDANT ENZYME AOE37-2. ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AI005184.1 GI:3214694
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS
TITLE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio-llnl.gov/bbrp/image/image.html
Insert Length: 1005 Std Error: 0.00
Seq primer: primer name ambiguous
High quality sequence stop: 1.
Location/Qualifiers

FEATURES
source

1..28
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1632169"

/sex="female, pooled"
 /tissue_type="breast"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Br2"
 /note="Vector: pTT3D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from pooled bulk
 breast tumor tissue, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pTT3
 vector. This library is the normalized version of
 NCI CGAP Br1.1. Library was constructed by Bento Soares
 and M. Fatima Bonaldo."

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGG 18
 ||| |||||
 Db 1 TTGAAGAAGCGG 13

RESULT 39

AA192663/c

LOCUS

DEFINITION zq03f12.s1 Stratagene muscle G37209 Homo sapiens cDNA clone
 IMAGE:628655 3' similar to TR:G556044 G556044 CYTOCHROME B ;, mRNA
 sequence.

ACCESSION

AA192663

VERSION

AA192663.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
 Martin, J., Moore, B., Schellenberg, K., Steptoe, N., Tan, F.,
 Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE

WASHU-NCI human EST Project

JOURNAL

Unpublished (1997)

COMMENT

Contact: Wilson RK
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Possible reversed clone: similarity on wrong strand

Insert Length: 825 Std Error: 0.00

Seq primer: -40M13 fwd. from AmerSham

High quality sequence stop: 1.

FEATURES

source

1..28 Location/Qualifiers

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GDB:5048889"

/db_xref="taxon:9606"

/clone="IMAGE:628655"

/tissue_type="muscle"

/dev_stage="adult"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Stratagene muscle 937209"

/note="Organ: skeletal muscle; Vector: pBluescript SK-;

Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally.

Primer: Oligo dT. Skeletal muscle from patient with

malignant hyperthermia. Average insert size: 1.0 Kb;

ORIGIN

Query Match 49.0%; Score 9.8; DB 1; Length 28;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 7 TGCAGGAAGCGG 19
 ||| |||||
 Db 15 TGTAGGAAGCGG 3

RESULT 40

AJ594066/c

LOCUS

DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
 392C12, genomic survey sequence.

ACCESSION

AJ594066

VERSION

AJ594066.1

KEYWORDS

GSS; left border; T-DNA flanking sequence.

SOURCE

Arabidopsis thaliana

ORGANISM

Arabidopsis thaliana

REFERENCE

AUTHORS

Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
 Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelleter, G.,
 Lepiniec, L., Caboche, M. and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences
 of pre-insertion sites

TITLE

EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
 Gaston Cremieux, 91057 Evry cedex, FRANCE
 PCR was performed on DNA from transformants of Arabidopsis thaliana
 plants from INRA (Versailles). The DNA fragment(s) resulting from
 the PCR were directly sequenced from the left or the right border
 to determine the genomic sequence flanking the insertion. T-DNA
 derived sequences were removed. Information to order the
 corresponding mutant line and a link to a database providing a
 graphical display of the insertion site are available at
 http://dbgap.versailles.inra.fr/publiclines/. This sequence has
 been generated in the framework of the French plant genomics
 program "Genoplatte" (http://www.genoplatte.com and
 http://genoplatte-info.infobiogen.fr).

FEATURES

source

1..29 Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="392C12"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Wassilewskija"

misc_feature 1..29

/note="T-DNA flanking sequence

left border"

ORIGIN

Query Match 49.0%; Score 9.8; DB 10; Length 29;
 Best Local Similarity 84.6%; Pred. No. 5.2e+06;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTGCAGGAA 14

|||||

Db 28 AATCTTGCGAGAA 16

Search completed: December 3, 2005, 15:07:09

Job time : 3655 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:17:55 ; Search time 137 Seconds
(without alignments)
259.498 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactcttcgaggaagcggt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 1026780

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*

- 1: /cgn2_6/ptodata/1/ina/1/COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5/COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A/COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B/COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H/COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PC/TUS/COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP/COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE/COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.8	74.0	25	3	US-09-396-196G-124305
C 2	14.2	71.0	25	3	US-09-396-196G-65325
C 3	14	70.0	20	3	US-09-288-461-19
C 4	14	70.0	20	3	US-09-758-881-19
C 5	13.8	69.0	28	3	US-08-137-134B-13
C 6	13.6	68.0	25	3	US-09-396-196G-3439
C 7	13.6	68.0	25	3	US-09-396-196G-42438
C 8	13.2	66.0	23	3	US-09-496-444-6
C 9	13.2	66.0	25	3	US-09-396-196G-40794
C 10	13.2	66.0	25	3	US-09-396-196G-65314
C 11	13.2	66.0	25	3	US-09-396-196G-88577
C 12	13.2	66.0	25	3	US-09-396-196G-88578
C 13	12.8	64.0	20	3	US-09-081-385-134
C 14	12.8	64.0	20	3	US-09-752-639-134
C 15	12.8	64.0	20	3	US-09-712-813-134
C 16	12.8	64.0	20	3	US-09-700-354A-134
C 17	12.8	64.0	25	3	US-09-396-196G-26683
C 18	12.8	64.0	25	3	US-09-396-196G-26684
C 19	12.8	64.0	25	3	US-09-396-196G-26685
C 20	12.8	64.0	25	3	US-09-396-196G-107676
C 21	12.8	64.0	25	3	US-09-396-196G-107677
C 22	12.8	64.0	25	3	US-09-396-196G-107678
C 23	12.8	64.0	25	3	US-09-396-196G-107679
C 24	12.8	64.0	25	3	US-09-396-196G-108203

ALIGNMENTS

RESULT 1

US-09-396-196G-124305/c

; Sequence 124305, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396.196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 124305

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-124305

Query Match 74.0%; Score 14.8; DB 3; Length 25;

Best Local Similarity 88.9%; Pred. No. 3.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGGACCG 18

Db 19 GGCTCTTCGAGGACGAG 2

RESULT 2

US-09-396-196G-65325

; Sequence 65325, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Mittmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affymetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396.196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

Sequence 30, Appl
Sequence 7, Appl
Sequence 86, Appl
Sequence 86, Appl
Sequence 86, Appl
Sequence 13006, A
Sequence 13007, A
Sequence 13008, A
Sequence 13009, A
Sequence 13010, A
Sequence 13011, A
Sequence 13012, A
Sequence 56156, A
Sequence 8, Appl
Sequence 77, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 79, Appl
Sequence 79, Appl

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; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65325
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65325

Query Match          71.0%; Score 14.2; DB 3; Length 25;
Best Local Similarity 84.2%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  2  ACTCTTCAGGAAGCGGCT 20
      ||||| ||| ||| |||
Db  5  ACTCTTCAGGAAGTGGCT 23

RESULT 3
US-09-288-461-19
; Sequence 19, Application US/09288461
; Patent No. 6159694
; GENERAL INFORMATION:
; APPLICANT: Kariras, James G.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0338
; CURRENT APPLICATION NUMBER: US/09/288,461
; CURRENT FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-09-288-461-19

Query Match          70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  GACTCTTGCAGGAA 14
      ||||| ||| |||
Db  7  GACTCTTGCAGGAA 20

RESULT 4
US-09-758-881-19
; Sequence 19, Application US/09758881
; Patent No. 6727064
; GENERAL INFORMATION:
; APPLICANT: Kariras, James G.
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0532
; CURRENT APPLICATION NUMBER: US/09/758,881
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-19

Query Match          70.0%; Score 14; DB 3; Length 20;
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```
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  GACTCTTGCAGGAA 14
      ||||| ||| |||
Db  7  GACTCTTGCAGGAA 20

RESULT 5
US-08-137-134B-13
; Sequence 13, Application US/08137134B
; Patent No. 6369038
; GENERAL INFORMATION:
; APPLICANT: BLUMENFELD, Marta
; APPLICANT: BRANDYS, Pascal
; APPLICANT: D'AURIOL, Luc
; APPLICANT: VASSEUR, Marc
; TITLE OF INVENTION: CLOSED SENSE AND ANTISENSE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN
; STREET: 400 Seventh Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,134B
; FILING DATE: 23-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/05114
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: PLAYER, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58359
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-137-134B-13

Query Match          69.0%; Score 13.8; DB 3; Length 28;
Best Local Similarity 88.2%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  3  CTCTTCAGGAAGCGGC 19
      ||| ||| ||| |||
Db  12 CTCTTCAGGAAGCGGC 28

RESULT 6
US-09-396-196G-3439/c
; Sequence 3439, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
```


; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; EARLIER FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3439
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-3439

Query Match 68.0%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGGAGCGGCT 20
||| ||||| |||||
Db 21 GAACCTTCGAGGAGCGTCT 2

RESULT 7
US-09-396-196G-42438
; Sequence 42438, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42438
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-42438

Query Match 68.0%; Score 13.6; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGGAGCGGCT 20
||| ||||| |||||
Db 4 GACTCTTCGAGGAGTAGTCT 23

RESULT 8
US-09-496-444-6/c
; Sequence 6, Application US/09496444
; Patent No. 6933376
; GENERAL INFORMATION:
; APPLICANT: Tao, Yumin
; APPLICANT: Gordon-Kamm William J.
; APPLICANT: Lowe, Keith S.
; APPLICANT: Bailey, Matthew A.
; TITLE OF INVENTION: Cell Cycle Polynucleotide, Polypeptide,
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 1109
; CURRENT APPLICATION NUMBER: US/09/496,444
; CURRENT FILING DATE: 2000-02-02
; EARLIER APPLICATION NUMBER: US 60/119,857
; EARLIER FILING DATE: 1999-02-12
; EARLIER APPLICATION NUMBER: US 60/101,551

; EARLIER FILING DATE: 1998-09-23
; EARLIER APPLICATION NUMBER: US 09/398,858
; EARLIER FILING DATE: 1999-09-20
; EARLIER APPLICATION NUMBER: US 09/257,131
; EARLIER FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: (1)...(23)
US-09-496-444-6

Query Match 66.0%; Score 13.2; DB 3; Length 23;
Best Local Similarity 83.3%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGGAAGCGGCT 20
||| ||||| |||||
Db 19 CTGTTGCAGCAAGCGGCT 2

RESULT 9
US-09-396-196G-40794/c
; Sequence 40794, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40794
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-40794

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTGCAGGAAGCGGCT 20
||| ||||| |||||
Db 20 CTATGGCTGGAGCGGCT 3

RESULT 10
US-09-396-196G-65314
; Sequence 65314, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65314
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-65314

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAAGCGGC 19
||||| ||| ||| ||| |||
Db 8 ACTCTTCAGGAAGTGGC 25

RESULT 11
US-09-396-196G-88577
; Sequence 88577, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88577
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88577

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAAGCGGC 19
||||| ||| ||| ||| |||
Db 5 AGTCTTCAGGAAGCAGC 22

RESULT 12
US-09-396-196G-88578
; Sequence 88578, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88578
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-88578

Query Match 66.0%; Score 13.2; DB 3; Length 25;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;

Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 ACTCTTCAGGAAGCGGC 19
||||| ||| ||| ||| |||
Db 2 AGTCTTCAGGAAGCAGC 19

RESULT 13
US-09-081-385-134
; Sequence 134, Application US/09081385
; Patent No. 6593456
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods
; TITLE OF INVENTION: of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,385
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/964,747
; FILING DATE: 05-NOV-1997
; APPLICATION NUMBER: 60/030,761
; FILING DATE: 06-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Wu, Frank
; REGISTRATION NUMBER: 41,386
; REFERENCE/DOCKET NUMBER: 22000-20577.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-081-385-134

Query Match 64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGC 19
||||| ||| ||| ||| |||
Db 1 TCTTCCAGGAAGGTGC 16

RESULT 14
US-09-752-639-134
; Sequence 134, Application US/09752639
; Patent No. 6911314
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; APPLICANT: Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; TITLE OF INVENTION: Factor Receptor Releasing Enzyme Activity, and Methods

;; TITLE OF INVENTION: of Use Thereof
;; NUMBER OF SEQUENCES: 154
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MORRISON & FOERSTER
;; STREET: 755 PAGE MILL ROAD
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304-1018
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: Windows
;; SOFTWARE: FastSEQ for Windows Version 2.0b
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/752,639
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US99/10793
;; FILING DATE:
;; APPLICATION NUMBER: 09/081,385
;; FILING DATE:
;; APPLICATION NUMBER: 08/964,747
;; FILING DATE: 05-NOV-1997
;; APPLICATION NUMBER: 60/030,761
;; FILING DATE: 06-NOV-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wu, Frank
;; REGISTRATION NUMBER: 41,386
;; REFERENCE/DOCKET NUMBER: 22000-20577.21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-813-5600
;; TELEFAX: 650-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; NAME: Wu, Frank
;; REGISTRATION NUMBER: 41,386
;; REFERENCE/DOCKET NUMBER: 22000-20577.21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-813-5600
;; TELEFAX: 650-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-09-752-639-134
Query Match 64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCTTCGAGGAGCGGC 19
Db 1 TCTTCGAGGAGCTGC 16
RESULT 15
US-09-712-813-134
; Sequence 134, Application US/09712813
; Patent No. 6930084
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, T.
; Granger, G.A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; Factor Receptor Releasing Enzyme Activity, and Methods
; of Use Thereof
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible

;; OPERATING SYSTEM: Windows
;; SOFTWARE: FastSEQ for Windows Version 2.0b
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/712,813
;; FILING DATE: 13-NOV-1997
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/081,385
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: 08/964,747
;; FILING DATE: 05-NOV-1997
;; APPLICATION NUMBER: 60/030,761
;; FILING DATE: 06-NOV-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Wu, Frank
;; REGISTRATION NUMBER: 41,386
;; REFERENCE/DOCKET NUMBER: 22000-20577.21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-813-5600
;; TELEFAX: 650-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; NAME: Wu, Frank
;; REGISTRATION NUMBER: 41,386
;; REFERENCE/DOCKET NUMBER: 22000-20577.21
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-813-5600
;; TELEFAX: 650-494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 134:
;; SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-09-712-813-134
Query Match 64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 TCTTCGAGGAGCGGC 19
Db 1 TCTTCGAGGAGCTGC 16
RESULT 16
US-09-700-354A-134
; Sequence 134, Application US/09700354A
; Patent No. 6955894
; GENERAL INFORMATION:
; APPLICANT: Gatanaga, Tetsuya
; Granger, Gale A.
; TITLE OF INVENTION: Factors Altering Tumor Necrosis
; Factor Receptor Releasing Enzyme Activity.
; NUMBER OF SEQUENCES: 154
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BOZICEVIC, FIELD, & FRANCIS, LLP
; STREET: 200 MIDDLEFIELD ROAD, #200
; CITY: Menlo Park
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/700,354A
; FILING DATE: 17-Apr-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/081,385
; FILING DATE: 14-MAY-1998
; APPLICATION NUMBER: PCT/US99/10793
; FILING DATE: 14-MAY-1999
; ATTORNEY/AGENT INFORMATION:
; NAME: Francis, Carol L.
; REGISTRATION NUMBER: 36,513

```
; REFERENCE/DOCKET NUMBER: IRVN-007CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-09-700-354A-134

Query Match          64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGC 19
Db 1 TCTTCCAGGAAGCTGC 16

RESULT 17
US-09-396-196G-26683/c
; Sequence 26683, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26683
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-26683

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGC 19
Db 25 TCGTCCAGGAAGCGGC 10

RESULT 18
US-09-396-196G-26684/c
; Sequence 26684, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26684

; REFERENCE/DOCKET NUMBER: IRVN-007CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-09-700-354A-134

Query Match          64.0%; Score 12.8; DB 3; Length 20;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGC 19
Db 1 TCTTCCAGGAAGCTGC 16

RESULT 17
US-09-396-196G-26683/c
; Sequence 26683, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26683
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-26683

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGC 19
Db 25 TCGTCCAGGAAGCGGC 10

RESULT 18
US-09-396-196G-26684/c
; Sequence 26684, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26684

; REFERENCE/DOCKET NUMBER: IRVN-007CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 134:
US-09-700-354A-134

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.5e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGC 19
Db 22 TCGTCCAGGAAGCGGC 7

RESULT 19
US-09-396-196G-26685/c
; Sequence 26685, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26685
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-26685

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGGC 19
Db 16 TCGTCCAGGAAGCGGC 1

RESULT 20
US-09-396-196G-107676/c
; Sequence 107676, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107676
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107676

Query Match          64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 GACTCTTCGAGGAGC 16
|||||
Db 25 GACTCTTCGATGTC 10

RESULT 21
US-09-396-196G-107677/c
; Sequence 107677, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107677
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107677

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGGAGC 16
|||||
Db 23 GACTCTTCGATGTC 8

RESULT 22
US-09-396-196G-107678/c
; Sequence 107678, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107678
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107678

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGGAGC 16
|||||
Db 22 GACTCTTCGATGTC 7

RESULT 23
US-09-396-196G-107679/c
; Sequence 107679, Application US/09396196G
; Patent No. 6821724

; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107679
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-107679

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTCGAGGAGC 16
|||||
Db 16 GACTCTTCGATGTC 1

RESULT 24
US-09-396-196G-108203/c
; Sequence 108203, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108203
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-108203

Query Match 64.0%; Score 12.8; DB 3; Length 25;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAGCGGCT 20
|||||
Db 17 CTTGAATGAGCGGCT 2

RESULT 25
US-09-972-115A-30
; Sequence 30, Application US/09972115A
; Patent No. 6599728
; GENERAL INFORMATION:
; APPLICANT: Geron Corporation
; APPLICANT: Gregg, Morin B.
; APPLICANT: Walter, Funk D.
; APPLICANT: Mieczyslaw, Piatyszek A.
; TITLE OF INVENTION: A Second Mammalian Telomerase
; FILE REFERENCE: 080/003C
; CURRENT APPLICATION NUMBER: US/09/972,115A
; CURRENT FILING DATE: 2001-10-05

;; PRIOR APPLICATION NUMBER: US 60/128,577
;; PRIOR FILING DATE: 2000-04-10
;; PRIOR APPLICATION NUMBER: US 60/129,123
;; PRIOR FILING DATE: 1999-04-13
;; NUMBER OF SEQ ID NOS: 64
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 30
;; LENGTH: 21
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Primer
US-09-972-115A-30

Query Match 63.0%; Score 12.6; DB 3; Length 21;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTTCAGGAAGCGC 19
||| |||| |||| ||
Db 3 GACAATTGCTGGAAGCTGC 21

RESULT 26
US-08-749-852-7
; Sequence 7, Application US/08749852
; Patent No. 5874222
; GENERAL INFORMATION:
; APPLICANT: JIRTLE, RANDY L.
; APPLICANT: DE SOUZA, ANGUS T.
; APPLICANT: HANKINS, GERALD R.
; TITLE OF INVENTION: TUMOR SUPPRESSOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P. C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/749,852
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-104
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-749-852-7

Query Match 63.0%; Score 12.6; DB 2; Length 22;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTTCAGGAAGCGC 19
||| |||| |||| ||
Db 4 GACTGTCCTGGAAGCAGC 22

RESULT 27
US-08-297-299B-86
; Sequence 86, Application US/08297299B
; Patent No. 5656427
; GENERAL INFORMATION:
; APPLICANT: Phillip Hammond and
; APPLICANT: Anthony Endozo
; TITLE OF INVENTION: NUCLEIC ACID HYBRIDI-
; ZATION ASSAY PROBES,
; TITLE OF INVENTION: HELPER PROBES AND
; TITLE OF INVENTION: AMPLIFICATION OLIGO-
; NUCLEOTIDES TARGETED TO
; TITLE OF INVENTION: MYCOPLASMA PNEUMONIAE
; TITLE OF INVENTION: NUCLEIC ACID
; NUMBER OF SEQUENCES: 92
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,299B
; FILING DATE: August 29, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: n/a
; FILING DATE: n/a
; ATTORNEY/AGENT INFORMATION:
; NAME: Heber, Sheldon O.
; REGISTRATION NUMBER: 38,179
; REFERENCE/DOCKET NUMBER: 208/130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-297-299B-86

Query Match 63.0%; Score 12.6; DB 2; Length 23;
Best Local Similarity 78.9%; Pred. No. 4.5e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACTCTTTCAGGAAGCGC 19
||||| ||||| ||||
Db 5 GACTCTAGCAGCAATGCG 23

RESULT 28
US-08-858-083-86
; Sequence 86, Application US/08858083
; Patent No. 5969122
; GENERAL INFORMATION:
; APPLICANT: Phillip Hammond and
; APPLICANT: Anthony Endozo
; TITLE OF INVENTION: NUCLEIC ACID HYBRIDI-
; ZATION ASSAY PROBES,
; TITLE OF INVENTION: NUCLEIC ACID HYBRIDI-
; ZATION ASSAY PROBES,


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; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13006
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13006

Query Match          63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGAGCGGCT 20
Db 7 AGTCCTGCCAGAGCGGCT 25

RESULT 31
US-09-866-108A-13007
; Sequence 13007, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13007
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13007

Query Match          63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGAGCGGCT 20
Db 6 AGTCCTGCCAGAGCGGCT 24

RESULT 32
US-09-866-108A-13008
; Sequence 13008, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13008
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13008

Query Match          63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGAGCGGCT 20
Db 5 AGTCCTGCCAGAGCGGCT 23

RESULT 33
US-09-866-108A-13009
; Sequence 13009, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
```


; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13009
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13009

Query Match 63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 ACTCTTGCGAGGCGGCT 20
Db 4 AGTCTGCCAGAGCGGCT 22

RESULT 34
US-09-866-108A-13010
; Sequence 13010, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13010
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13010

Query Match 63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 ACTCTTGCGAGGCGGCT 20
Db 3 AGTCTGCCAGAGCGGCT 21

RESULT 35
US-09-866-108A-13011
; Sequence 13011, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharon G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEWICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13011
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13011

Query Match 63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 2 ACTCTTGCGAGGCGGCT 20
Db 3 AGTCTGCCAGAGCGGCT 21

```
Db      2 AGTCTGCCAGAGCGGCT 20

RESULT 36
US-09-866-108A-13012
; Sequence 13012, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: ABOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 15755
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 13012
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-13012

Query Match      63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db      1 AGTCTGCCAGAGCGGCT 19

Query Match      63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db      1 AGTCTGCCAGAGCGGCT 19

RESULT 37
US-09-396-196G-56156
; Sequence 56156, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 56156
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-56156

Query Match      63.0%; Score 12.6; DB 3; Length 25;
Best Local Similarity 78.9%; Pred. No. 4.6e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 ACTCTTGCGAGAGCGGCT 20
        ||||| ||||| ||||| |||||
Db      7 ACTCTTACGAAAGCGGCT 25

RESULT 38
US-09-449-335-8
; Sequence 8, Application US/09449335
; Patent No. 6303365
; GENERAL INFORMATION:
; APPLICANT: Busch, Marco
; APPLICANT: Hain, Rudiger
; APPLICANT: Martin, William
; APPLICANT: Tietjen, Klaus
; APPLICANT: Kloti, Andreas
; TITLE OF INVENTION: Method of determining the activity of
; TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate reductoisomerase and
; FILE REFERENCE: 2020US
; CURRENT APPLICATION NUMBER: US/09/449,335
; CURRENT FILING DATE: 1999-11-24
; EARLIER APPLICATION NUMBER: DE 199 35 967.9
; PRIOR APPLICATION NUMBER: 1999-07-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-449-335-8

Query Match      63.0%; Score 12.6; DB 3; Length 30;
Best Local Similarity 78.9%; Pred. No. 4.7e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GACTCTTGCGAGAGCGGC 19
        ||||| ||||| ||||| |||||
Db      8 GACTCATGATGAAGTGGC 26

RESULT 39
US-08-171-718-77/c
; Sequence 77, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Guseella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,718
FILING DATE: 22-DEC-1993
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,034
FILING DATE: 25-FEB-1993
APPLICATION DATA:
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 0609.3850003
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-171-718-77

Query Match 62.0%; Score 12.4; DB 2; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CTCTTGACGAGGC 16
||| ||||| |||
Db 15 CTCITGACGGTAGC 2

RESULT 40
US-08-478-087-77/c
Sequence 77, Application US/08478087
Patent No. 6077685
GENERAL INFORMATION:
APPLICANT: Trofatter, James A.
APPLICANT: MacCollin, Mia M.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,087
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/171,718
FILING DATE: 22-DEC-1993
APPLICATION NUMBER: US 08/108,808
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/022,034

FILING DATE: 25-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/026,063
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 0609.3850003
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-087-77
Query Match 62.0%; Score 12.4; DB 3; Length 20;
Best Local Similarity 92.9%; Pred. No. 5.6e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 CTCTTGACGAGGC 16
||| ||||| |||
Db 15 CTCITGACGGTAGC 2
Search completed: December 3, 2005, 15:09:35
Job time : 138 secs

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:22:14 ; Search time 796 Seconds
(without alignments)
207.773 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactcttgacgagcgcgct 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134699005 residues

Total number of hits satisfying chosen parameters: 10535742

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications NA_Main:
- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
 - 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:
 - 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:
 - 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
 - 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:
 - 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
 - 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
 - 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:
 - 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:
 - 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	9	US-10-773-678-342
2	20	100.0	29	9	US-10-773-678-158
3	19	95.0	20	9	US-10-773-678-179
4	19	95.0	20	9	US-10-773-678-341
5	18	90.0	20	9	US-10-773-678-343
6	17	85.0	20	9	US-10-773-678-340
7	17	85.0	20	9	US-10-773-678-344
8	16.4	82.0	25	9	US-10-956-157-186717
9	16	80.0	20	9	US-10-857-715-201
10	15.2	76.0	25	9	US-10-956-157-301412
11	15.2	76.0	25	10	US-10-060-756-287536
12	15	75.0	20	9	US-10-773-678-339
13	15	75.0	20	9	US-10-773-678-345
14	14.8	74.0	25	7	US-10-719-956-135575
15	14.8	74.0	25	7	US-10-719-956-196148
16	14.8	74.0	25	8	US-10-719-900-191405
17	14.8	74.0	25	9	US-10-809-189-124305
18	14.8	74.0	25	9	US-10-956-157-205933
19	14.4	72.0	25	8	US-10-719-900-611442
20	14.4	72.0	25	9	US-10-956-157-178444
21	14.4	72.0	25	10	US-11-036-317-95537
22	14.2	71.0	21	8	US-10-751-736-54782
23	14.2	71.0	25	7	US-10-719-956-51664

24	14.2	71.0	25	9	US-10-809-189-65325	Sequence 65325, A
25	14.2	71.0	25	10	US-11-036-317-193968	Sequence 193968, A
26	14.2	71.0	25	10	US-11-036-317-247028	Sequence 247028, A
27	14.2	71.0	25	10	US-11-036-317-255809	Sequence 255809, A
28	14.2	71.0	25	10	US-11-036-317-289853	Sequence 289853, A
29	14.2	71.0	25	10	US-11-036-317-308860	Sequence 308860, A
30	14.2	71.0	25	10	US-11-036-317-435916	Sequence 435916, A
31	14.2	71.0	25	10	US-11-036-317-473142	Sequence 473142, A
32	14.2	71.0	25	10	US-11-036-317-482672	Sequence 482672, A
33	14.2	71.0	25	10	US-11-036-317-538007	Sequence 538007, A
34	14.2	71.0	25	10	US-11-036-317-634153	Sequence 634153, A
35	14.2	71.0	25	10	US-11-036-317-648448	Sequence 648448, A
36	14.2	71.0	25	10	US-11-036-317-773627	Sequence 773627, A
37	14.2	71.0	25	10	US-11-036-317-940292	Sequence 940292, A
38	14.2	71.0	25	10	US-11-036-317-975516	Sequence 975516, A
39	14	70.0	20	3	US-09-758-881-19	Sequence 19, Appl
40	14	70.0	20	9	US-10-773-678-19	Sequence 19, Appl
41	14	70.0	25	7	US-10-719-956-410880	Sequence 410880, A
42	14	70.0	25	8	US-10-719-900-718599	Sequence 718599, A
43	14	70.0	25	10	US-11-036-317-649659	Sequence 649659, A
44	13.8	69.0	21	8	US-10-751-736-54781	Sequence 54781, A
45	13.8	69.0	21	8	US-10-751-736-54784	Sequence 54784, A

ALIGNMENTS

RESULT 1
US-10-773-678-342
; Sequence 342, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773.678
; PRIOR FILING DATE: 2004-02-06
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2003-11-14
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 342
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-342
Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GACTCTTGACGAGCGGCT 20
Db 1 GACTCTTGACGAGCGGCT 20
RESULT 2
US-10-773-678-158/c
; Sequence 158, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3

```
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Probe
US-10-773-678-158
```

```
Query Match 100.0%; Score 20; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GACTCTTGCAGGAAGCGCT 20
    |||||
Db 26 GACTCTTGCAGGAAGCGCT 7
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RESULT 3

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US-10-773-678-179
; Sequence 179, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
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; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 179
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-179
```

```
Query Match 95.0%; Score 19; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GACTCTTGCAGGAAGCGC 19
    |||||
Db 2 GACTCTTGCAGGAAGCGC 20
```

RESULT 4

```
US-10-773-678-341
; Sequence 341, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 341
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-341
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Query Match 95.0%; Score 19; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 ACTCTTGCAGGAAGCGCT 20
    |||||
Db 1 ACTCTTGCAGGAAGCGCT 19
```

RESULT 5

```
US-10-773-678-343
; Sequence 343, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
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```
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 343
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-343
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Query Match 90.0%; Score 18; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 GACTCTTGCAGGAAGCGG 18
    |||||
Db 3 GACTCTTGCAGGAAGCGG 20
```

RESULT 6

```
US-10-773-678-340
```

; Sequence 340, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 340
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-340

Query Match 85.0%; Score 17; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGGCT 20
|||||
Db 1 TCTTGCAGGAGCGGCT 17

RESULT 7
US-10-773-678-344
; Sequence 344, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 344
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-344

Query Match 85.0%; Score 17; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCG 17
|||||
Db 4 GACTCTTCAGGAGCG 20

RESULT 8
US-10-956-157-186717/c
; Sequence 186717, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 186717
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-186717

Query Match 82.0%; Score 16.4; DB 9; Length 25;
Best Local Similarity 94.4%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAGCGG 18
|||||
Db 20 GACTCTTCAGGAGGGG 3

RESULT 9
US-10-857-715-201
; Sequence 201, Application US/10857715
; Publication No. US20050164218A1
; GENERAL INFORMATION:
; APPLICANT: Agus David
; APPLICANT: Baker Joffre
; APPLICANT: Natale Ron
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Gene Expression Markers for Response to
; FILE REFERENCE: 39740/0011
; CURRENT APPLICATION NUMBER: US/10/857,715
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/474,908
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: reverse primer
US-10-857-715-201

Query Match 80.0%; Score 16; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTTGCAGGAGCGGCT 20
|||||
Db 1 CTTGCAGGAGCGGCT 16

RESULT 10
US-10-956-157-301412/c
; Sequence 301412, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

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; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 301412
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-301412

Query Match          76.0%; Score 15.2; DB 9; Length 25;
Best Local Similarity 85.0%; Pred. No. 8.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGCGGCT 20
Db 23 GCCTTTCGACGAAGCGGCT 4

RESULT 11
US-11-060-756-287536/c
; Sequence 287536, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drg
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060.756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 287536
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe
US-11-060-756-287536

Query Match          76.0%; Score 15.2; DB 10; Length 25;
Best Local Similarity 85.0%; Pred. No. 8.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAGCGGCT 20
Db 23 GCCTTTCGACGAAGCGGCT 4

RESULT 12
US-10-773-678-339
; Sequence 339, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karraas, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773.678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 339
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-135575
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-339

Query Match          75.0%; Score 15; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TTGCAGGAAGCGGCT 20
Db 1 TTGCAGGAAGCGGCT 15

RESULT 13
US-10-773-678-345
; Sequence 345, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karraas, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773.678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 345
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense oligonucleotide
US-10-773-678-345

Query Match          75.0%; Score 15; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAAG 15
Db 6 GACTCTTGCAGGAAG 20

RESULT 14
US-10-719-956-135575/c
; Sequence 135575, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 135575
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-135575
```



```
Query Match      74.0%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 ACTCTTGAGGAGCGGC 19
    ||||| ||||| |||||
Db  22 ACTCGTGAGGATGCGGC 5

RESULT 15
US-10-719-956-196148
; Sequence 196148, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 196148
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-196148

Query Match      74.0%; Score 14.8; DB 7; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 ACTCTTGAGGAGCGGC 19
    ||||| ||||| |||||
Db  7 ACTCTTGCTGTAAGCGGC 24

RESULT 16
US-10-719-900-181405/c
; Sequence 181405, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 181405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-181405

Query Match      74.0%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 ACTCTTGAGGAGCGGC 19
    ||||| ||||| |||||
Db  22 ACTCGTGAGGATGCGGC 5

RESULT 17
US-10-809-189-124305/c
; Sequence 124305, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
```

```
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 124305
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-124305

Query Match      74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  1 GACTCTTGACGAGGCGG 18
    ||||| ||||| |||||
Db  19 GGCTCTTGACGAGGCGG 2

RESULT 18
US-10-956-157-205933/c
; Sequence 205933, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 205933
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-205933

Query Match      74.0%; Score 14.8; DB 9; Length 25;
Best Local Similarity 88.9%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2 ACTCTTGAGGAGCGGC 19
    ||||| ||||| |||||
Db  18 ACTCTTGAGGAGCGGC 1

RESULT 19
US-10-719-900-611442/c
; Sequence 611442, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 611442
; LENGTH: 25
```

```
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-611442

Query Match      72.0%; Score 14.4; DB 8; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CTTGCAGGAGCGGCT 20
   |||||
Db 19 CTTGCAGGAGCAGCT 4

RESULT 20
US-10-956-157-178444/c
; Sequence 178444, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 178444
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
US-10-956-157-178444

Query Match      72.0%; Score 14.4; DB 9; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CTTGCAGGAGCGGCT 20
   |||||
Db 21 CTTCCAGGAGCGGCT 6

RESULT 21
US-11-036-317-95537/c
; Sequence 95537, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 95537
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-95537

Query Match      72.0%; Score 14.4; DB 10; Length 25;
Best Local Similarity 93.8%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TCTTGACGAGGAGCGGC 19
   |||||
Db 20 TCGTGACGAGGAGCGGC 5

RESULT 22
US-10-773-678a-342.max30.rnpbm

US-10-751-736-54782/c
; Sequence 54782, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; PRIOR FILING DATE: 2003-01-06
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54782
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNai
US-10-751-736-54782

Query Match      71.0%; Score 14.2; DB 8; Length 21;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACTCTTGACGAGGAGCGGCT 20
   |||||
Db 21 AATCTTCTAGGAGCGGCT 3

RESULT 23
US-10-719-956-51664/c
; Sequence 51664, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 51664
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-51664

Query Match      71.0%; Score 14.2; DB 7; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 ACTCTTGACGAGGAGCGGCT 20
   |||||
Db 20 ACTCTTACAGGAGCGGCT 2

RESULT 24
US-10-809-189-65325
; Sequence 65325, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
```

; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65325
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-10-809-189-65325

Query Match 71.0%; Score 14.2; DB 9; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACTCTTCAGGAAGCGGCT 20
Db 5 ACTCTTCAGGAAGTGCT 23

RESULT 25

US-11-036-317-193968
; Sequence 193968, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:

; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 193968
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-193968

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAAGCGGC 19
Db 5 GACCCCTGCAGGAAGTGCC 23

RESULT 26

US-11-036-317-247028
; Sequence 247028, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:

; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 247028
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-247028

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAAGCGGC 19
Db 3 GACCCCTGCAGGAAGTGCC 21

RESULT 27

US-11-036-317-255809
; Sequence 255809, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:

; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 255809
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-255809

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAAGCGGC 19
Db 2 GACCCCTGCAGGAAGTGCC 20

RESULT 28

US-11-036-317-289853
; Sequence 289853, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:

; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 289853
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-289853

Query Match 71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACTCTTCAGGAAGCGGC 19
Db 1 GACCCCTGCAGGAAGTGCC 19

RESULT 29

US-11-036-317-308860
; Sequence 308860, Application US/11036317
; Publication No. US20050214823A1


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RESULT 34
US-11-036-317-634153/c
; Sequence 634153, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 634153
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-634153

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 2 ACTCTTCGAGGAGCGGCT 20
    ||||| ||||| |||||
Db 21 ATTCTCGAGCAGCGGCT 3

RESULT 35
US-11-036-317-648448
; Sequence 648448, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 648448
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-648448

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 GACTCTTCGAGGAGCGGC 19
    ||||| ||||| |||||
Db 1 GACTCTTCGAGGAGCGGC 19

RESULT 36
US-11-036-317-773627
; Sequence 773627, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
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; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 773627
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-773627

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 GACTCTTCGAGGAGCGGC 19
    ||||| ||||| |||||
Db 6 GACTCTTCGAGGAGCGGC 24

RESULT 37
US-11-036-317-940292
; Sequence 940292, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 940292
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-940292

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 2 ACTCTTCGAGGAGCGGCT 20
    ||||| ||||| |||||
Db 7 ACTCTTCGAGGAGCGGCT 25

RESULT 38
US-11-036-317-975516
; Sequence 975516, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 975516
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-975516

Query Match          71.0%; Score 14.2; DB 10; Length 25;
Best Local Similarity 84.2%; Pred. No. 2.7e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 GACTCTTCGAGGAGCGGC 19
```

Db 2 GACTACTGCAGCGGC 20
||||| ||||| |||||

RESULT 39
US-09-758-881-19
; Sequence 19, Application US/09758881
; Patent No. US20010029250A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0532
; CURRENT APPLICATION NUMBER: US/09/758,881
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-881-19

Query Match 70.0%; Score 14; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAA 14
Db 7 GACTCTTGCAGGAA 20
||||| ||||| |||||

RESULT 40
US-10-773-678-19
; Sequence 19, Application US/10773678
; Publication No. US20050074879A1
; GENERAL INFORMATION:
; APPLICANT: Karras, James G
; TITLE OF INVENTION: Antisense Oligonucleotide Modulation of STAT3
; TITLE OF INVENTION: Expression
; FILE REFERENCE: ISPH-0828
; CURRENT APPLICATION NUMBER: US/10/773,678
; CURRENT FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 10/713,139
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 09/758,881
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/09054
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 09/288,461
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 402
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-773-678-19

Query Match 70.0%; Score 14; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTCTTGCAGGAA 14
||||| ||||| |||||

Db 7 GACTCTTGCAGGAA 20

Search completed: December 3, 2005, 15:23:05
Job time : 796 secs

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November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases; older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions **.rapbn** (Published Applications_NA_Main) and **.rapbn** (Published Applications_NA_New).
Searches run against Amino Acid Published Applications produce two sets of results, with the extensions **.rapbm** (Published Applications_AA_Main) and **.rapbm** (Published Applications_AA_New).

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OM nucleic - nucleic search, using sw model

Run on: December 3, 2005, 13:30:06 ; Search time 233 Seconds
(without alignments)
26.714 Million cell updates/sec

Title: US-10-773-678A-342

Perfect score: 20

Sequence: 1 gactctgcaggagcggt 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6442102

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
And is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	80.0	20	7	US-11-102-228-233
C 2	14.4	72.0	19	8	US-11-101-244-1290351
C 3	14.4	72.0	19	9	US-11-083-784-1290351
C 4	13.8	69.0	19	8	US-11-101-244-439270
C 5	13.8	69.0	19	9	US-11-083-784-439270
C 6	13.4	67.0	19	8	US-11-101-244-1290317
C 7	13.4	67.0	19	9	US-11-083-784-1290317
C 8	13.2	66.0	19	8	US-11-101-244-556327
C 9	13.2	66.0	19	9	US-11-083-784-556327
10	13	65.0	19	8	US-11-101-244-968731
11	13	65.0	19	8	US-11-101-244-968803
12	13	65.0	19	9	US-11-101-244-1066415
13	13	65.0	19	8	US-11-083-784-968731
14	13	65.0	19	9	US-11-083-784-968803
15	13	65.0	19	9	US-11-083-784-1066415
C 16	12.8	64.0	19	8	US-11-101-244-21319
C 17	12.8	64.0	19	8	US-11-101-244-1169015
C 18	12.8	64.0	19	8	US-11-101-244-1552463
C 19	12.8	64.0	19	8	US-11-101-244-1585494
C 20	12.8	64.0	19	9	US-11-083-784-21319
C 21	12.8	64.0	19	9	US-11-083-784-1169015
C 22	12.8	64.0	19	9	US-11-083-784-1552463
C 23	12.8	64.0	19	9	US-11-083-784-1585494

24	12.8	64.0	22	6	US-10-750-185-14564	Sequence 14564, A
C 25	12.6	63.0	20	7	US-11-090-739-13	Sequence 13, Appl
C 26	12.4	62.0	19	8	US-11-101-244-251435	Sequence 251435, A
C 27	12.4	62.0	19	8	US-11-101-244-251481	Sequence 251481, A
C 28	12.4	62.0	19	8	US-11-101-244-1337482	Sequence 1337482, A
C 29	12.4	62.0	19	9	US-11-083-784-251435	Sequence 251435, A
C 30	12.4	62.0	19	9	US-11-083-784-251481	Sequence 251481, A
C 31	12.4	62.0	19	9	US-11-083-784-1337482	Sequence 1337482, A
C 32	12.2	61.0	19	8	US-11-101-244-186562	Sequence 186562, A
C 33	12.2	61.0	19	8	US-11-101-244-199830	Sequence 199830, A
C 34	12.2	61.0	19	8	US-11-101-244-266845	Sequence 266845, A
C 35	12.2	61.0	19	8	US-11-101-244-266905	Sequence 266905, A
C 36	12.2	61.0	19	8	US-11-101-244-277581	Sequence 277581, A
C 37	12.2	61.0	19	8	US-11-101-244-487058	Sequence 487058, A
C 38	12.2	61.0	19	8	US-11-101-244-726311	Sequence 726311, A
C 39	12.2	61.0	19	8	US-11-101-244-855529	Sequence 855529, A
C 40	12.2	61.0	19	8	US-11-101-244-1268245	Sequence 1268245, A
C 41	12.2	61.0	19	8	US-11-101-244-1268345	Sequence 1268345, A
C 42	12.2	61.0	19	8	US-11-101-244-1270630	Sequence 1270630, A
C 43	12.2	61.0	19	8	US-11-101-244-145586	Sequence 145586, A
C 44	12.2	61.0	19	8	US-11-101-244-1511826	Sequence 1511826, A
C 45	12.2	61.0	19	8	US-11-101-244-1531334	Sequence 1531334, A

ALIGNMENTS

RESULT 1
US-11-102-228-233
; Sequence 233, Application US/11102228
; Publication No. US20050260646A1
; GENERAL INFORMATION:
; APPLICANT: BAKER, JOFFRE B.
; APPLICANT: SHAK, STEVEN
; APPLICANT: GIANNI, LUCA
; TITLE OF INVENTION: GENE EXPRESSION MARKERS FOR PREDICTING
; TITLE OF INVENTION: RESPONSE TO CHEMOTHERAPY
; FILE REFERENCE: 39740-0017
; CURRENT APPLICATION NUMBER: US/11/102.228
; CURRENT FILING DATE: 2005-04-07
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Reverse Primer
US-11-102-228-233

Query Match 80.0%; Score 16; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CTTGAGGAGCGGCT 20
|||||
Db 1 CTTGAGGAGCGGCT 16

RESULT 2
US-11-101-244-1290351/c
; Sequence 1290351, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101.244

; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1290351
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1290351

Query Match 72.0%; Score 14.4; DB 8; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGC 19
|||||
Db 16 TCTTGCAGGAAGCAGC 1

RESULT 3

US-11-083-784-1290351/c
; Sequence 1290351, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1290351
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1290351

Query Match 72.0%; Score 14.4; DB 9; Length 19;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAAGCGC 19
|||||
Db 16 TCTTGCAGGAAGCAGC 1

RESULT 4

US-11-101-244-439270/c
; Sequence 439270, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S

; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 439270
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-439270

Query Match 69.0%; Score 13.8; DB 8; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGGAAGCGG 18
|||||
Db 17 ACTCTTGAGGGAAGCGG 1

RESULT 5

US-11-083-784-439270/c
; Sequence 439270, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 439270
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-439270

Query Match 69.0%; Score 13.8; DB 9; Length 19;
Best Local Similarity 88.2%; Pred. No. 2.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGACGGAAGCGG 18
|||||
Db 17 ACTCTTGAGGGAAGCGG 1

RESULT 6

US-11-101-244-1290317/c
; Sequence 1290317, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 134990S

```

; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1290317
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1290317

```

```

Query Match 67.0%; Score 13.4; DB 8; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 6 TTGCAGGAAGCGGCT 20
    ||||| ||||| |||
Db 19 TTGCAGGAAGCAGCT 5

```

```

RESULT 7
US-11-083-784-1290317/c
; Sequence 1290317, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1290317
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1290317

```

```

Query Match 67.0%; Score 13.4; DB 9; Length 19;
Best Local Similarity 93.3%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 6 TTGCAGGAAGCGGCT 20
    ||||| ||||| |||
Db 19 TTGCAGGAAGCAGCT 5

```

```

RESULT 8
US-11-101-244-556327/c
; Sequence 556327, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

```

```

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 556327
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-556327

```

```

Query Match 66.0%; Score 13.2; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 2 ACTCTTCAGGAAGCGGC 19
    ||||| ||||| |||
Db 18 ACTCTTCAGGAGCTGC 1

```

```

RESULT 9
US-11-083-784-556327/c
; Sequence 556327, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 556327
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-556327

```

```

Query Match 66.0%; Score 13.2; DB 9; Length 19;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

Qy 2 ACTCTTCAGGAAGCGGC 19
    ||||| ||||| |||
Db 18 ACTCTTCAGGAGCTGC 1

```

```

RESULT 10
US-11-101-244-968731
; Sequence 968731, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```

```
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 968731
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-968731
```

```
Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 6.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 TCTTGCAGGAAGC 16
Db 3 UCUGCAGGAAGC 15
```

```
RESULT 11
US-11-101-244-968803
; Sequence 968803, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 968803
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-968803
```

```
Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 6.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 TCTTGCAGGAAGC 16
Db 3 UCUGCAGGAAGC 15
```

```
RESULT 12
US-11-101-244-1066415
; Sequence 1066415, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
```

```
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1066415
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1066415
```

```
Query Match 65.0%; Score 13; DB 8; Length 19;
Best Local Similarity 92.3%; Pred. No. 6.7e+02;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 8 GCAGGAAGCGGCT 20
Db 1 GCAGGAAGCGGCU 13
```

```
RESULT 13
US-11-083-784-968731
; Sequence 968731, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 968731
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-968731
```

```
Query Match 65.0%; Score 13; DB 9; Length 19;
Best Local Similarity 76.9%; Pred. No. 6.7e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 TCTTGCAGGAAGC 16
Db 3 UCUGCAGGAAGC 15
```

```
RESULT 14
US-11-083-784-968803
; Sequence 968803, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
```

RESULT 16
US-11-101-244-21319/c
; Sequence 21319, Application US/11101244
; Publication No. US2005024679A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

RESULT 18
US-11-101-244-1552463/c
; Sequence 1552463, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

; SEQ ID NO 1552463
; LENGTH: 19

; TYPE: RNA
; ORGANISM: Homo sapiens

US-11-101-244-1552463

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ACTCTTGCAGGAGCG 17
|||||
Db 19 ACTCATGCGAGTGGC 4

RESULT 19

US-11-101-244-1585494/c

; Sequence 1585494, Application US/11/101244
; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

; SEQ ID NO 1585494
; LENGTH: 19

; TYPE: RNA
; ORGANISM: Homo sapiens

US-11-101-244-1585494

Query Match 64.0%; Score 12.8; DB 8; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGC 16
|||||
Db 19 GAATCTGGCAGGAGC 4

RESULT 20

US-11-083-784-21319/c

; Sequence 21319, Application US/11/083784
; Publication No. US20050245475A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

; SEQ ID NO 21319
; LENGTH: 19

; TYPE: RNA
; ORGANISM: Homo sapiens

US-11-083-784-21319

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TCTTGCAGGAGCGC 19
|||||
Db 17 TCTTGAAGGAGTGGC 2

RESULT 21

US-11-083-784-1169015/c

; Sequence 1169015, Application US/11/083784
; Publication No. US20050245475A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary

; SEQ ID NO 1169015
; LENGTH: 19

; TYPE: RNA
; ORGANISM: Homo sapiens

US-11-083-784-1169015

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACTCTTGCAGGAGC 16
|||||
Db 19 GAATCTGGCAGGAGC 4

RESULT 22

US-11-083-784-1552463/c

; Sequence 1552463, Application US/11/083784
; Publication No. US20050245475A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1552463
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1552463

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 ACTCTTGCAGGAGCG 17
Db 19 ACTCATGCAGGATGCG 4

RESULT 23
US-11-083-784-1585494/c
; Sequence 1585494, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacoon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1585494
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1585494

Query Match 64.0%; Score 12.8; DB 9; Length 19;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GACTCTTGCAGGAGCG 16
Db 19 GAATCTGCAGGAGCG 4

RESULT 24
US-10-750-185-14564
; Sequence 14564, Application US/10750185

; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 14564
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Reverse Primer
US-10-750-185-14564

Query Match 64.0%; Score 12.8; DB 6; Length 22;
Best Local Similarity 87.5%; Pred. No. 8.6e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 ACTCTTGCAGGAGCG 17
Db 7 ACTCTTGCAGGAGCG 22

RESULT 25
US-11-090-739-13/c
; Sequence 13, Application US/11090739
; Publication No. US20050260639A1
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, Yusuke
; APPLICANT: KATAGIRI, Toyomasa
; APPLICANT: NAKAGAWA, Hirowaki
; TITLE OF INVENTION: METHOD FOR DIAGNOSING PANCREATIC CANCER
; FILE REFERENCE: 082368-003600US
; CURRENT APPLICATION NUMBER: US/11/090,739
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: PCT/JP2003/011817
; PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/555,809
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/450,889
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/414,872
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 13
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Artificially synthesized primer sequence for RT-PCR
US-11-090-739-13

Query Match 63.0%; Score 12.6; DB 7; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 ACTCTTGCAGGAGCGGCT 20
Db 20 AATCTCCAGGAGCTGCT 2

RESULT 26

US-11-101-244-251435/c
; Sequence 251435, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 251435
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-251435

Query Match 62.0%; Score 12.4; DB 8; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||
Db 18 ACTCTTGCAGGTAG 5

RESULT 27

US-11-101-244-251481/c
; Sequence 251481, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 251481
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-251481

Query Match 62.0%; Score 12.4; DB 8; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||
Db 17 ACTCTTGCAGGTAG 4

RESULT 28

US-11-101-244-1337482/c
; Sequence 1337482, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1337482
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1337482

Query Match 62.0%; Score 12.4; DB 8; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||
Db 18 ACTCTTGCAGGAAG 5

RESULT 29

US-11-083-784-251435/c
; Sequence 251435, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 251435
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-251435

Query Match 62.0%; Score 12.4; DB 9; Length 19;
Best Local Similarity 92.9%; Pred. No. 1.4e+03;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15
|||||
Db 18 ACTCTTGCAGGTAG 5

RESULT 30

US-11-083-784-251481/c
; Sequence 251481, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784

; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333

; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 251481

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-083-784-251481

Query Match 62.0%; Score 12.4; DB 9; Length 19;

Best Local Similarity 92.9%; Pred. No. 1.4e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15

|||||

Db 17 ACTCTTGCAGGTAG 4

RESULT 31

US-11-083-784-1337482/c
; Sequence 1337482, Application US/11083784
; Publication No. US20050245475A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/083,784

; CURRENT FILING DATE: 2005-03-18

; PRIOR APPLICATION NUMBER: US/10/714,333

; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 1337482

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-083-784-1337482

Query Match 62.0%; Score 12.4; DB 9; Length 19;

Best Local Similarity 92.9%; Pred. No. 1.4e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACTCTTGCAGGAAG 15

|||||

Db 17 ACTCTTGCAGGTAG 4

Db

18 ACTCTTGCAGAAAG 5

RESULT 32

US-11-101-244-186562/c
; Sequence 186562, Application US/11101244
; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244

; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 186562

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-101-244-186562

Query Match 61.0%; Score 12.2; DB 8; Length 19;

Best Local Similarity 82.4%; Pred. No. 1.7e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAGCGGCT 20

|||||

Db 19 TCTTGCAGGAAACCGGT 3

RESULT 33

US-11-101-244-199830/c
; Sequence 199830, Application US/11101244
; Publication No. US20050246794A1

; GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.

; APPLICANT: Khvorova, Anastasia

; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin

; APPLICANT: Marshall, William

; APPLICANT: Scaringe, Stephen

; TITLE OF INVENTION: Functional and Hyperfunctional siRNA

; FILE REFERENCE: 13499US

; CURRENT APPLICATION NUMBER: US/11/101,244

; CURRENT FILING DATE: 2005-04-07

; PRIOR APPLICATION NUMBER: 60/502,050

; PRIOR FILING DATE: 2003-09-10

; PRIOR APPLICATION NUMBER: 60/426,137

; PRIOR FILING DATE: 2002-11-14

; NUMBER OF SEQ ID NOS: 1591911

; SOFTWARE: Proprietary

; SEQ ID NO 199830

; LENGTH: 19

; TYPE: RNA

; ORGANISM: Homo sapiens

US-11-101-244-199830

Query Match 61.0%; Score 12.2; DB 8; Length 19;

Best Local Similarity 82.4%; Pred. No. 1.7e+03;

Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCTTGCAGGAGCGGCT 20

|||||

Db 19 TCATGCAGCAAGTGGCT 3

RESULT 34

US-11-101-244-266845/c
; Sequence 266845, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 266845
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-266845

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTCGAGGAGCGGC 19
||| ||||| |||||
Db 17 CTCTTCGAGGAGCGGC 1

RESULT 35

US-11-101-244-266905/c
; Sequence 266905, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 266905
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-266905

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CTCTTCGAGGAGCGGC 19
||| ||||| |||||
Db 17 CTCTTCGAGGAGCGGC 1

RESULT 36

US-11-101-244-277581/c
; Sequence 277581, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 277581
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-277581

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTCGAGGAGCGGCT 20
||| ||||| |||||
Db 19 TCATTCAGGATCGGCT 3

RESULT 37

US-11-101-244-487058/c
; Sequence 487058, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmakon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 487058
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-487058

Query Match 61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TCTTCGAGGAGCGGCT 20
||| ||||| |||||
Db 19 TCATTCAGGATCGGCT 3

RESULT 38

```
US-11-101-244-726311/c
; Sequence 726311, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 726311
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-726311
```

```
Query Match          61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 4 TCTTCAGGAGCGGCT 20
    |||||
Db 19 TCTTCAGGAGCGGCT 3
```

RESULT 39

```
US-11-101-244-855529/c
; Sequence 855529, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 855529
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-855529
```

```
Query Match          61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 4 TCTTCAGGAGCGGCT 20
    |||||
Db 18 TGTTCAGGAGAGGCT 2
```

RESULT 40

```
US-11-101-244-1268245/c
; Sequence 1268245, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1268245
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1268245
```

```
Query Match          61.0%; Score 12.2; DB 8; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.7e+03;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 3 CTCTTCAGGAGCGGC 19
    |||||
Db 17 CTGTTTCAGGAGCTGC 1
```

Search completed: December 3, 2005, 15:27:10
Job time : 234 secs

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